us-09-719-379a-5.rai

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100.0%; Score 107; DB 2;
ilarity 100.0%; Pred. No. 1.7e-10;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local Simi
Matches 19;
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13, Appli

135, Appli

135, Appli
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                                                                                                                  (without alignments)
75.324 Million cell updates/sec
                                                                                                  November 24, 2004, 09:14:14 ; Search time 16.7283 Seconds
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Patent No. 53
Sequence 541
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Sequence 2,
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Sequence 2
Sequence 2
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Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 US-08-460-502-10
3 US-09-148-711A-10
1 US-09-457-997B-2
1 US-08-467-722A-2
1 US-09-411-184-2
1 US-09-148-711A-1
1 US-09-148-711A-1
1 US-09-148-711A-1
1 US-09-148-711A-1
1 US-09-148-711A-1
1 US-09-148-711A-1
1 US-09-148-71A-1
2 US-09-718-692-4
US-09-718-692-4
US-09-718-692-4
US-09-718-692-2
US-09-718-852-2
                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                         478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Perfect score:
                                                                                                                                                                                                                                       Scoring table:
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107
107
101
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Maximum DB E
                                                                  OM protein
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                                                                                                  Run on:
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Sequence 2, Appli
Sequence 1753, A
Sequence 18, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 2760, A
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 16380, A
Sequence 4656, Ap
Sequence 6229, A
Sequence 6229, A
Sequence 6229, A
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Sequence 10. Application US/08460502

Patent No. S843464

JAPLICANT: Bakaletz, Lauren O.
APPLICANT: Raumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: 00. Superior Avenue
STREE: 00. S.A.
STREE: 100. S.A.
STREE: 100. S.A.
STREE: 100. S.A.
STREE: 100. S.A.
STREE: 00. Superior Avenue
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STREE: 00. Superior Avenue
STREE: 00. S.A.
STREE: 00. S.A.
STREE: 00. S.A.
STREE: 00. SUPERIOR STREET STREET
US-08-463-461-2
US-09-248-796A-17753
US-08-867-941-18
US-09-074-658-18
US-09-074-658-14
US-09-074-658-15
US-09-074-658-15
US-09-074-658-15
US-09-074-658-15
US-09-134-001C-5471
US-09-134-001C-5471
US-09-134-001C-678-18
US-09-248-796A-16380
US-09-248-796A-16380
US-09-270-767-49094
US-09-107-512A-6229
US-09-252-991A-26646
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     single
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STRANDEDNESS: si
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Gaps

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Length 40; Indela 138 RSDYKFYEDANGTRDHKKG 156

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US-09-148-711A-10

Sequence 10, Application US/09148711A

Sequence 10, Application US/09148711A

Patent No. 6436405

TITLE APPLICANT: The Ohio State University

TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

FILE REFERENCE: 1852-04010

CURRENT FILIGE DATE: 1998-09-04

PRIOR PILICATION NUMBER: US/09/148,711A

PRIOR PLICATION NUMBER: 09/460,502

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.0

LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 107; DB 4; Length 40; 100.0%; Pred. No. 1.7e-10; Live 0; Mismatches 0; Indels
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Sequence 2, Application US/08457997B

Patent No. 5766608

GENERAL INFORMATION:

FAPPLICANT: Kolattukudy, P. E.

TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calfee, Halter and Griswold
STATE: Ohio

CITY: Cleveland
STATE: Ohio

COUNTRY: U.S.A.

ZIP: 44114-2688

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IB PC compatible

OPERATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURSSIFICATION NUMBER: US/08/457,997B

FILING DATE:

CLASSIFICATION NUMBER: 34,829

REGISTRATION NUMBER: 34,829

REGISTRATION NUMBER: 22777/00102

TELECPHONE: (216) 622-8450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSDYKFYEDANGTRDHKKG 19
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TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i: 359 amino acids
amino acid
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Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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US-08-457-997B-2
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Sequence 2, Application US/09451184

Patent No. 6562349

GENERAL INFORMATION:

APPLICANT: Kolattukudy, P. B.

TITLE OF INVENTION:

OCRESPONDENCES: 6

CORRESPONDENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: 1400 McDonald Investment Center,

STREET: 800 Superior Avenue

CITY: Cleveland

STATE: Ohio

COUNTRY: U.S.A>

LIP: 44114-2688

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PED POCOMPATIONE

COMPUTER: PED POCOMPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ohio
COUNTRY: U.S.A>
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PACHON HIS
COMPUTER: PACHON HIS
COMPUTER: PACHON NOWBER: US/08/467,722A
PILING SYSTEM: US/08/467,722A
PILING DATE:
CLASSIFICATION NUMBER: US/08/467,722A
ATTORNEY/AGENT INFORMATION:
NAME: GOLILCK, MATY E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELECHONE: (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                   Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OP INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSDYKFYEDANGTRDHKKG 19
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INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 359 amino acida
amino acid
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Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-722A-2
US-08-467-722A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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Sequence 1, Application US/09148711A

Sequence 1, Application US/09148711A

GENERAL INFORMATION:

APPLICANT: The Ohio State University

TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

FILE REFERENCE: 18525-04010

CURRENT APPLICATION NUMBER: US/09/148,711A

CURRENT FILING DATE: 1998-09-04

PRIOR APPLICATION UNMBER: 08/460,502

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.4%; Score 101; DB 4; Length 18;
100.0%; Pred. No. 6.4e-10;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Harrington, James J
REFERENCE/DOCKET NUMBER: 32,144
TELECOMMUNICATION INFORMATION:
TELEFAX: 201/831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                 1 RSDYKFYEDANGTRDHKK 18
      1 RSDYKFYEDANGTRDHKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Haemophilus influenza
US-09-148-711A-1
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TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                          US-09-148-711A-1
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Patent No. 5843464

GENERAL INFORMATION:
APPLICANT: Bakaletz, Lauren O.
APPLICANT: Raumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Pimbrin Peptides
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 107; DB 4; Length 359; 100.0%; Pred. No. 2e-09; tive 0; Mismatches 0; Indels (
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,502
                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24547/04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8416
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22727/00120
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/451,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: GOLICK, MAY E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 RSDYKFYEDANGTRDHKKG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSDYKFYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 359 amino acids
rypE: amino acids
rypE: amino acid
ropology: linear
ropology: linea
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Best Local Similarity 100.C
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-460-502-1
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Gapв

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Best Local Similarity 47.1
Matches 8, Conservative
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Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                        LENGTH
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5352450-2
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Patent No. 6024958
GENERAL INFORMATION: Thomas
APPLICANT: Lebner, Thomas
APPLICANT: Lebner, Thomas
APPLICANT: Lebner, POLYPEPTIDE FRAGMENTS CAPABLE
TITLE OF INVENTION: OF COMPETITION WITH STREPTOCOCCUS MUTANS ANTIGEN I/II
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                         ö
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                                                              Length 338;
                                                                                                                      4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Washington STREET: 2000 Pennsylvania Avenue, NW, suite 5500 CITY: Washington STATE: DCCCUNTRY: USA
ZIP: 2000 Fennsylvania Avenue, NW, suite 5500 STATE: DCCCUNTRY: USA
ZIP: 20006-1888
COMPUTER READBLE FORM: WINGOWS VERBION TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: Windows Version 2.0b CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/894,017
FILING DATE: 31-JUL-1997
CLASSIFICATION NUMBER: PCT/GB96/00207
FILING DATE: 31-JUL-1997
FILING DATE: 31-JAN-1996
ATTORNEY/AGENT INFORMATION: NUMBER: WIASHING NUMBER: WASHING NUMBER: WASHIN
                                                           Score 79; DB 1; 1
Pred. No. 6.4e-05;
                                     73.8%; Scc.
78.9%; Pred. No. ...
0; Mismatches
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Patent No. 6500433
GENERAL INFORMATION
APPLICANT: Lehner, Thomas
APPLICANT: Kelly, Charles
                                                                                                                                                                                                                 1 RSDYKFYEDANGTRDHKKG 19
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SEQUENCE CHARACTERISTICS:
LENGTH: 1561 amino acids
                                                                                                                      Conservative
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Matches 8; Conservative
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MOLECULE TYPE: protein
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STRANDEDNESS: 817
                                                           Query Match
Best Local Similarity
Matches 15; Conserv
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US-09-456-474-23
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US-08-210-394-1
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Sequence 5419, Application US/09328352

Retent No. 6562958

GENERAL INFORMATION:
APPLICANT: GETY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5419
LENGTH: 442
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TITLE OF INVENTION: POLYPEPTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: COMPETITION WITH STREPTOCOCCUS MUTANS ANTIGEN I/II
FILE REFERENCE: 25150-20067.10
CURRENT APPLICATION NUMBER: 105/99/456,474
CURRENT FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 08/894,017
PRIOR APPLICATION NUMBER: US 08/894,017
PRIOR PILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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; APPLICANT: KOCA, TOSHIHIKO; OKAHASHI, NOBUO; TAKAHASHI, ICHIRO;

; SHIBUYA, KOJI; OHTA, HIROTAKA

; TITLE OF INVENTION: METHOD FOR PREPARING VACCINE FOR DENTAL

; CARIES AND VACCINAL COMPOSITIONS FOR DENTAL CARIES USED AS NASAL
                                                                                                                                                                                                                                                                                                                                                                                                              43.9%; Score 47; DB 4; Length 1561; 47.1%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1565;
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41.6%; Score 44.5; DB 4;
Best Local Similarity 47.8%; Pred. No. 34;
Matches 11; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%; Score 47; DB 6; 47.1%; Pred. No. 56; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/529,602
FILING DATE: 29-MAY-1990
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US-09-328-352-5419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1377 EYNFYDDYDQTGDHYTG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| ||:| : | || |
1382 EYNFYDDYDQTGDHYTG 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 DYKFYEDANGTRDHKKG 19
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                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-456-474-23
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID, NO 4.
LENGTH: 366
TYPE: PRT
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; Patent No. 5942386
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                                                                                                                                                                40.2%;
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Best Local Similarity 50.v.
Best Local 8; Conservative
                                                                                                                                              Query Match
Best Local Similarity 66...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                  166 RSNIKIHEDANG 177
                                                                                                                                                                                                                                            1 RSDYKFYEDANG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-621-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                     ) ORGANISM: Human
US-09-718-815-4
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                                                                                                 Sequence 4, Application US/09718692
| Ratent No. 538796
| GENERAL INFORMATION:
| APPLICANT: Beraud, Christophe
| APPLICANT: Freedman, Richard
| TITLE OF INVENTION: No. 53879661 motor proteins and methods for
| TITLE OF INVENTION: their use
| TITLE REFERENCE: 1052
| CURRENT APPLICATION UNDBER: US/09/718,692
| CURRENT FILING DATE: 2000-11-22
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: FASTSEQ for Windows Version 4.0
| SEQ ID NO 4
| LENGTH: 366
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Patent No. 6426193
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6426193e1 motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 1052
CURRENT APPLICATION NUMBER: US/09/718,852
CURRENT PILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6455293
GENERAL INFORMATION:
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6455293e1 motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 1052
CURRENT APPLICATION NUMBER: US/09/718,815
CURRENT PILING DATE: 2000-11-22
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          36 FVEDANGSILFRIGYLTRDKKQG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-718-815-4
                                                                 RESULT 13
US-09-718-692-4
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US-09-718-852-4
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                                                                                                                               Gaps
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      Length 366;
                                                                                                                               Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Gerhold, David L.
APPLICANT: Gerhold, David L.
APPLICANT: Gerhold, David L.
APPLICANT: Strauss, Allyson Cole
TITLE OF INVENTION: Anti-fungal Agents and Methods of
TITLE OF INVENTION: Identifying and Using the Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5691187ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: U.S.A.
ZIP: 19103
ZIP: 19103
ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM YEB: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,621
Score 43; DB 4;
Pred. No. 49;
2; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
RESISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TOJU-1584
TELECHONE: 215-568-3100
TELEFAX: 215-568-3100
TE
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; Patent No. 5691187
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Gaps
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Patent No. 6383796
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TITLE OF INVENTION: No. 6383796e1 motor proteins and methods for
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09718852
Patent No. 6426193
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Freedman, Richard
TILE OF INVENTION: No. 6426193el motor proteins and methods for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.2%; Score 43; DB 5; Length 780; 50.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
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CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                    PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/485,621
FILING DATE: 07-UNN-1995
CLASSIFICATION DATA:
APPLICATION WUMBER: US 60/000,399
FILING DATE: 21-JUN-1995
CLASSIFICATION NUMBER: 33,229
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUU-1970
TELECHOME: 215-568-3190
TELECHOME: 215-568-3190
                 APPLICATION NUMBER: PCT/US96/09530A
                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-568-343,
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :||:| :| | ||
382 QSDFKKFETARKLRDH 397
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Best Local Similarity 50.07
Matches 8; Conservative
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171 RSNIKIHEDANG 182
CURRENT APPLICATION DATA:
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US96-09530A-2
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US-09-718-852-2
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GENERAL INFORMATION:
APPLICANT: Kaniec, Eric B.
APPLICANT: Strauss, Allyson Cole
TITLE OF INVENTION: Identifying and Using the Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
        APPLICANT: Kniec, Eric B.
APPLICANT: Gerhold, David L.
APPLICANT: Gerhold, David L.
APPLICANT: Strauss, Allyson Cole
APPLICANT: Strauss, Allyson Cole
TITLE OF INVENTION: Identifying and Using the Same
TITLE OF INVENTION: Identifying and Using the Same
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5942386ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.2%; Score 43; DB 2; Length 780; 50.0%; Pred. No. 1.1e+02; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1584
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3139
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/973,83:
                                                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,621
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: PhilauciansTATE: Pennsylvania
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Matches 8; Conserva
GENERAL INFORMATION:
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PCT-US96-09530A-2
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Sequence 16049, Application US/09248796A

Sequence 16049, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR PEDLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16049

LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (433), (444)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-16049
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US-09-081-385-154

i Sequence 154, Application US/09081385

j Patent No. 6533456

j GENERAL INFORMATION:

APPLICANT: Gatanaga, T.

APPLICANT: Granger, G.A.

TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods

TITLE OF INVENTION: of Use Thereof

NUMBER OF SEQUENCES: 154

CORRESPONDENCE MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPATION SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,385
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Pred. No. 89;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
        3 DYKFYEDANGTRDHKK 18
                                       58 DHKFDEETTTNRDHFK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.3%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Parent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT APPLICATION NUMBER: US/09/198,452A
SEQ ID NOS: 6849
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; Sequence 2, Application US/09718815
; Retent No. 6455293
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Breadman, Richard
; TITLE OF INVENTION: their use
; FILE REFERENCE: 1052
; CURRENT FILING DATE: 2000-11-22
; UNMBER OF SEQ ID NOS: 4
; SQOTWARE: FREESEQ for Windows Version 4.0
; FILE NO NOS: 4
; SEQ ID NO 2: 4
; SEQ ID NO 3: 4
; SEQ ID NO 4: 6-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.2%; Score 43; DB 4; Length 1637;
66.7%; Pred. No. 2.6e+02;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%; Score 42; DB 4; Length 189; S0.0%; Pred. No. 34; tive 2; Mismatches 6; Indels
TITLE OF INVENTION: their use
FILE REFERENCE: 1052
CURRENT APPLICATION NUMBER: US/09/718,852
CURRENT FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TYPE: PRT
2 ORGANISM: Chlamydia pneumoniae
US-09-198-452A-135
                                                                                                                                                                                                                                                                                                                                                                           171 RSNIKIHEDANG 182
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Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||: | :|||||
171 RSNIKIHEDANG 182
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Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                           8; Conservative
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                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 22
US-09-198-452A-135
                                                                                                                                                         LENGTH: 1637
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APPLICANT: Fowler, Timothy
APPLICANT: Barnett, Christopher C.
APPLICANT: Shoemaker, Sharon
TITLE OF INVENTION: Saccharification of Cellulose by Cloning
TITLE OF INVENTION: and Amplification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Trichoderma Reesei
TITLE OF INVENTION: Trichoderma Reesei
TITLE OF INVENTION: Trichoderma Reesei
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
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TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
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TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Amblification of TITLE OF INVENTION OF INVE
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,080B
FILING DATE: 05-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: 06/248,586
FILING DATE: 24 MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/807,028
FILING DATE: 10-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/625,140
FILING DATE: 10-DEC-1990
CLASSIFICATION:
RAPPLICATION NUMBER: 07/625,140
FILING DATE: 10-DEC-1990
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: G778D3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,090
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08462090; Patent No. 6022725; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ::||| | :: |
589 DYKHFDDANITPRYEFG 605
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Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 744 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-462-080B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
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Patent No. 5997913

GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Shoemaker, Sharon
TITLE OF INVENTION: Saccharification of Cellulose by Cloning and
TITLE OF INVENTION: Amplification of the Beta-glucosidase Gene of Trichoderma Rees
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
CITTLE OF THE CORRESPONDENCE ADDRESS CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

FILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 4; I
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%; Scc.
50.0%; Pred. No. ...
0; Mismatches
                                                     41,386
ER: 22000-20577.21
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; Sequence 14256, Application US/09248796A
; Patent No. 6747137
        NAME: Wu, Frank
REGISTRATION NUMBER: 41,386
REFERENCE/DCKET NUMBER: 22006
TELECOMMUNICATION INFORMATION:
TELEPAN: 650-494-0792
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 693 amino acids
TYPE: amino acids
US-09-081-385-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 KLDRSFLEDTTPARDEKK 415
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56 SDYKYYDTTEPTSD 69
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US-09-248-796A-14256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity 50.0
Matches 7; Conservative
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COUNTRY: U.S.A.
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 26
US-08-462-080B-2
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RESULT 29

US-09-246-796A-17753

US-09-246-796A-17753

US-09-246-796A-17753

Sequence 17753, Application US/09248796A

Retent No. 6747137

GENERAL INFORMATION:

TITLE OF INVENTION: WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WOMBER: US/09/248,796A

CURRENT APPLICATION WUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

WUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (21)
COTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno US-09-248-796A-17753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Loosmore, Sheena M
APPLICANT: Dosmore, Sheena M
APPLICANT: Dosmore, Sheena M
APPLICANT: Wang, Yan.-Pan
APPLICANT: Wang, Yan.-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.3%; Score 41; DB 4; Length 756; 50.0%; Pred. No. 2.3e+02; tive 1; Mismatches 7; Indels
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CITY: Toroncy
STATE: Ontario
STATE: Ontario
STATE: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PREENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
TING DATE: 03-UUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael 1
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/08867941
Patent No. 5977337
GENERAL INFORMATION:
                                                                  3 DYKFYEDANGTRDHKKG 19
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Best Local Similarity 50.01
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Candida albicans
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APPLICANT: Barnett, Christopher C.
APPLICANT: Shoemaker, Shazon
TITLE OF INVENTION: Saccharification of the Beta-glucosidase Gene of
TITLE OF INVENTION: Trichoderma Reesei
TITLE OF INVENTION DATE: Trichoderma Reesei
TITLE OF TRICHOLOGY ASSOFTMARE: DESCRIPTION TRICHOLOGY ASSOFTMARE: DESCRIPTION TRICHOLOGY ASSOFTMARE: US/08/463,461
FILING DATE: OS-JUN-1995
TITLE OF TITLE OF TRICHOLOGY ASSOFTMARES
TRICHOLOGY ASSOFTMARENT TRICHOLOGY ASSOFTMARES
TRICHOLOGY ASSOFTMARENT TRICHOLOGY ASSOFTMARES
TRICHOLOGY ASSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.3%; Score 41; DB 3; Length 744; 47.1%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
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                            US 07/625,140
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NAME: Christopher L. Scone
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC78D4
TELEPHONE: 415-846-7555
TELEPAX: 415-846-7555
                      APPLICATION NUMBER: US 07/625
PILING DATE: 10-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: D111Ahuntv, T. Gene
REGISTRATION NUMBER: 25,423
REPERENCE/DOCKET NUMBER: 01001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08463461
Patent No. 6103464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 DYKHFDDANITPRYEFG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 744 amino acida TYPE: amino acid TYPE: amino acid TYPE: MOLECULE TYPE: protein US-08-463-461-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DYKFYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                                         TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 744 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-090-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.1'
Matches 8; Conservative
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Best Local Similarity 47.1
Matches 8; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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US-08-463-461-2
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Gaps

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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Run-Pan Du
APPLICANT: Run-Pan Du
APPLICANT: Run-Pan Du
APPLICANT: Run-Pan Du
APPLICANT: Vang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESSED: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
COUNTY: Canada
ZIP: MSG 1R7
COMPUTER REABBLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                   37.9%; Score 40.5; DB 2; Length 538; 35.7%; Pred. No. 1.9e+02; Live 3; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vergion #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION 1435
ATTORNEY/AGENT INFORMATION:
NAME: SLEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUTICATION INFORMATION:
TELEPHONE: (416) 595-1165
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TTELEPAX: Amino acids
                                                                                                                                                                                                                                                                                                                                                   310 DGKFYDDKSHNELAVFAHAGLRKDHQKG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09074658
Patent No. 6184371
GENERAL INFORMATION:
               TELEPHONE: (416) 595-1155
TELEPRAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 538 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-867-941-18
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
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RESULT 32

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APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Mang, Van-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Xang, Yan-Ping
APPLICANT: Right, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCRITANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09074658
Patent No. 6184371
GENERAL INPORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.9%; Score 40.5; DB 2; Length 541; 35.7%; Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,941
FILING DATE: 03-UUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart. Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
TELECOMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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Sequence 14, Application US/08867941; Patent No. 5977337; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 35.7
hes 10; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-867-941-14
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US-09-074-658-14
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LOGOMORE, Sheena M
APPLICANT: Run-Pan Du
APPLICANT: Run-Pan Du
APPLICANT: Vang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sin & MeBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                   COMPUTER FLEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION HAR-1998
CLASSIFICATION WINSER: 24,973
REFERENCE/DOCKET WINBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUTCATION INFORMATION:
TELEFHONE: (416) 595-1155
TELECOMMUTCATION INFORMATION:
TELEFHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2432 amino acids
TELEGTH: 2432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658 FILING DATE: 08-MAY-1998 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973 REPRENENCE/DOCKET NUMBER: 1038-795 TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.9%; Score 40.5; DB 3 Best Local Similarity 35.7%; Pred. No. 1e+03; Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2204 DGKFYDDKSHNELAVFAHAGLRKDHQKG 2231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09074658
Patent No. 6184371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                        COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                 Ontario
7: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT: GEATY L. Breton et al.
APPLICANT: GEATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2205-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
LENGTH: 544
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Patent No. 6184371
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan Ping
APPLICANT: Yang, Yan Ping
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michal H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.9%; Score 40.5; DB 3; Length 541; Best Local Similarity 35.7%; Pred. No. 1.9e+02; Matches 10; Conservative 3; Mismatches 4; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.9%; Score 40.5; DB 4; Length 544; 35.7%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING BATE: US-09/09/074,658
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARRCTERISTICS:
LENGTH: 541 main a caids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 DGKFYDDKSHNELAVFAHAGLRKDHQKG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DYKFYED-----ANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DYKFYED------ANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-540-236-2760
; Sequence 2760, Application US/09540236
; Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 35.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: bu..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 35
US-09-074-658-15
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Fadelact No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 322;
   Indels
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M
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Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 3.
   Mismatches
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                                                                                                                                                                                                                                                                             Sequence 13, Application US/09566076; Patent No. 6475775; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSDYKQYHDTTINGVSTDK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKFYEDA--NGTRDHK 17
      4.
                                                                                                 |:| :| |||:: |
250 FHELSNATRDYQPG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| :| |||:: |
250 FHELSNATRDYQPG 263
                                                          6 FYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 FYEDANGTRDHKKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.6
Matches 10; Conservative
   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-566-076-13
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Sequence 13, Application US/09080855A

Patent No. 6083721

GENERAL INFORMATION:

APPLICANT: Saras, Jan

APPLICANT: Franzn, Petra

APPLICANT: Heldina, Usf

APPLICANT: Heldina, Carl-Henrik

TILE REFERENCE: Locat-Henrik

TILE REFERENCE: Locat-Henrik

TILE REFERENCE: Locat-Henrik

CURRENT APPLICATION NUMBER: US/09/080, 855A

CURRENT APPLICATION NUMBER: US/09/080, 855A

CURRENT FILING DATE: 1998-05-18

EARLIER FILING DATE: 1998-05-18

EARLIER FILING DATE: 1997-02-25

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn WOLEST ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-108
PRIOR FILING DATE: 1997-108
RUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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                                                                                                                                                                                  Query Match 37.9%; Score 40.5; DB 3; Length 2439; Best Local Similarity 35.7%; Pred. No. 1e+03; Matches 10; Conservative 3; Mismatches 4; Indels 11.
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                                                                                                                                                                                                                                                                                                                                                 2211 DGKFYDDKSHNELAVFAHAGLRKDHQKG 2238
                                                                                                                                                                                                                                                                                                                 3 DYKFYED-----ANGTRDHKKG 19
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Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5471
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50.0%;
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   2439 amino acids
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                                                i TOPOLOGY: Bingle j TOPOLOGY: linear US-09-074-658-11
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CORGANISM: Homo sapiens
US-09-080-855-13
                         TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
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US-09-134-001C-5471
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Job time : 17.7283 secs

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Sequence 3, Appli
Sequence 7, Appli
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Sequence 5, Appli
Sequence 5, Appli
Sequence 53280, A
Sequence 145844,
Sequence 171844, Ap
Sequence 171824,
Sequence 171824,
Sequence 199530,
Sequence 199530,
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                                                                                                                            ; Search time 49.0326 Seconds (without alignments) 94.040 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-203-942-7
US-10-223-711-1
US-10-203-942-1
US-10-223-711-10
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US-10-282-122A-50359
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US-10-424-599-145844
US-10-424-599-171824
US-10-424-599-171824
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                                                                                                                                                                                                                                                                                                                                                                 1575965 seqs, 354694765 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Match Length
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Sequence:
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No.
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ALIGNMENTS

RESULT

Gaps

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APPLICANT: DENOEL, FANTELPEE
APPLICANT: DENOEL, PHILIPPE
APPLICANT: POOLMAN, JAN
APPLICANT: POOLMAN, JAN
APPLICANT: TOOLMAN, JAN
TITLE OF INVENTION: HAENOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REPERENCE: B45210
CURRENT PILLING DATE: 2002-08-15
PRIOR PELICATION NUMBER: PCT/EP01/01556
PRIOR PILLING DATE: 2001-02-13
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
SOFTWARE: FASELSC for Windows Version 4.0
SEQ ID NO 5
LENGTH: 28
APPLICANT: POOLMAN, JAN
APPLICANT: THONNARD, JOELLE
JITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REPERENCE: B45210
CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE FABELSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 14; Length 19;
Pred. No. 3.7;
2; Mismatches 0; Indels
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; Sequence 10, Application US/10223711
; Sequence 10, Application US/10223711
; Sequence 10, Application No. US20030113344A1
; GENERAL INFORMATION:
; APPLICANT: Bakaletz, Lauren O.
; APPLICANT: Kaumaya, Pravin T.P.
; TITLE OP INVENTION: Synthetic Chimeric Fimbrin Peptides
; FILE REFERENCE: 18525/04058
; CURRENT APPLICATION NUMBER: US/10/223,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB :
Pred. No. 5.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10203942
Publication No. US20030096370A1
GENERAL INFORMATION:
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DENOEL, PHILIPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Haemophilus influenzae
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77.8%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 7/...
7, Conservative
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0
                            Sequence 7, Application US/10203942

Publication No. US2030096370A1

GENERAL INFORMATION:

APPLICANT: BERTHET, FRANCOIS-XAVIER

APPLICANT: DENOEL, PHILIPPE

APPLICANT: POLIMAN, JAN

APPLICANT: POLIMAN, JAN

APPLICANT: POLIMAN, JAN

APPLICANT: POLIMAN, JOSELLE

TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION

FILE REFERENCE: B45210

CURRENT APPLICATION NUMBER: US/10/203,942

CURRENT FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: PCT/EP01/01556

PRIOR APPLICATION NUMBER: G8 0003502.2

PRIOR PILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 72; DB 14; Length 22; Best Local Similarity 100.0%; Pred. No. 8.6e-05; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%; Score 43; DB 14; Length 18; 77.8%; Pred. No. 3.5; tive 2; Mismatches 0; Indels
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i Sequence 1, Application US/10223711

j Sequence 1, Application US/10223711

j Publication No. USZ0030113344A1

j GENERAL INFORMATION:

APPLICANT: Bakaletz, Lauren O.

APPLICANT: Kaumaya, Pravin T.P.

TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

FILE REFERENCE: 18525/04058

CURRENT FILING DATE: 2002-08-19

PRIOR APPLICATION NUMBER: 09/148,711

PRIOR PILING DATE: 1998-09-04

PRIOR FILING DATE: 1995-06-02

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-203-942-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Haemophilus influenzae
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1 RSDYKFYED 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps

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; NAME/KEY: MISC_FEATURE
; LOCATION: (617)...(617)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-50359
                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                          JS-10-282-122A-53280
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                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                          DB 14;
                                                                                                                                                                                          Score 43; DB 1
Pred. No. 7.8;
2; Mismatches
                                                                                                                                                                                                                                                                                                                   US-10-282-122A-50359
; Sequence 50359, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION;
                                                                                                                                                 ) OTHER INFORMATION: synthetic construct US-10-223-711-10
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/148,711
PRIOR FILING DATE: 1998-09-04
PRIOR PILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 10
LENGTH: 40
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Burkholderia mallei
FEATURE:
                                                                                                                                                                                         Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                           1 RSDYKFYDN 9
                                                                                                                                                                                                                                                           | | | | | | | | | ::
1 RSDYKFYED 9
                                                                                                                             ORGANISM: Artificial
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CURRENT FILING DATE: 2003-02-20

FRIOR PAPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR FILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Traw.ck, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yorsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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Pred. No. 1.5e+02;
1; Mismatches 2; Indels
Score 43; DB 15; Length 696;
Pred. No. 1.4e+02;
                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 51280, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Clostridium difficile
US-10-282-122A-53280
        59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.3%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                               ||||: : |: :|
133 RSDYRIFQNRSVD 145
                                                                                                                                                              1 RSDYKFYDNKRID 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.0
7, Conservative
                                                                                     Conservative
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Gaps

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US-10-287-274-440

i Sequence 440, Application US/10287274

j Sequence 440, Application US/10287274

j Publication No. US20030181408A1

j GENERAL INFORMATION:

APPLICANT: Porsyth, R. Allyn

APPLICANT: Syskind, Judith

TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO

TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO

FILE REFERENCE: ELITAN 1008101

CURRENT FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: US 60/164415

PRIOR PILING DATE: 1099-11-09

PRIOR FILING DATE: 1099-11-09

PRIOR FILING DATE: 1099-11-09

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 440

LENGTH: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinha
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Dlants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 199530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%; Score 40; DB 17; Length 418; ilarity 54.5%; Pred. No. 2.5e+02; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                         Length 216;
                                                                                                                                                                                                                        3; Indels
                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_126171C.1.pep
US-10-424-599-171824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: MRT4577_113545C.1.pep
US-10-425-115-199530
                                                                                                                                                                            Score 40; DB 15;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(418)
OTHER_INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 199530, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                         Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                : || ||||||
176 KDDYPGYDNKR 186
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185 TNYKYYTNKRM 195
                                                                                                                                                                                                                                                                    1 RSDYKFYDNKR 11
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                    LENGTH: 216
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-10-425-115-199530
SEQ ID NO 171824
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                       Sequence 145844, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SPERIENTS: 38-21(53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENDIGH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 171824, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Road Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%; Score 40; DB 14; Length 46; 58.3%; Pred. No. 27; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_102716C.1.pep
US-10-424-599-145844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-10-083-357-1044
US-10-083-357-1044
; Sequence 1044, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
; APPLICANT: Olandong Zeng et al.
; TITLE OF INVENTION: Systemic Discovery of New Genes
; FILE REFERENCE: 032796-090
; CURRENT APPLICATION NUMBER: US/10/083,357
; CURRENT FILLING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 1346
; LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 15;
Pred. No. 34;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.8'
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSDYKFYDNKRI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RSDYKFYDN 9
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-10-424-599-171824
                    -10-424-599-145844
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APPLICANT: Xu, H.

TITLE OP INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PLILOR DATE: 2000-05-23

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/230,335

PRIOR PELICATION NUMBER: 60/230,347

PRIOR PELICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/257,635

PRIOR APPLICATION NUMBER: 60/257,635

PRIOR APPLICATION NUMBER: 60/257,635

PRIOR APPLICATION NUMBER: 60/257,636

PRIOR APPLICATION NUMBER: 60/257,636

PRIOR APPLICATION NUMBER: 60/257,636

PRIOR APPLICATION NUMBER: 60/257,636

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR APPLICATION NUMBER: 60/259,3
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                                                                                                                                            Score 40; DB 14; Length 437;
Pred. No. 2.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.6%; Score 40; DB 15; Length 437; 85.7%; Pred. No. 2.6e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12714, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Carlos
APPLICANT: Andlone, Carlos
APPLICANT: Andlone, Carlos
APPLICANT: Andlone, Carlos
APPLICANT: Obleen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamanoto, Robert
APPLICANT: Yerryth, R.
                                                                                                                                                Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-287-274-440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                          367 DYKYYDN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 DYKYYDN 373
                                                                                                                                                                                                                                                                                            3 DYKFYDN 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-10-282-122A-42714
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US-10-282-122A-42714
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APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Frawick, John
APPLICANT: Frawick, John
APPLICANT: Frawick, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERBNCE: ELITRA, 0344
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 06/19), 078
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-2-16
PRIOR PILING DATE: 2000-11-2-16
PRIOR PILING DATE: 2000-12-16
PRIOR PILING DATE: 2000-13-1
PRIOR PILING DATE: 2000-13-1
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Sequence 74928, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-282-122A-73481
; Sequence 73481, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Salmonella typhimurium US-10-282-122A-74928
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 DYKYYDN 373
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RESULT 15

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US-10-767-701-45949

US-10-767-701-45949

is Sequence 45949, Application US/10767701

j Publication No US20040172684A1

i GENERAL INCOMMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 45949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Sola, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 307322
Gaps
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1; Indels
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US-10-767-701-45949
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US-10-425-115-307322
3; Mismatches
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Best Local Similarity 77.8
Fest Local 7; Conservative
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Best Local Similarity 77.0
Best Local 7; Conservative
  6; Conservative
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ORGANISM: Sorghum bicolor
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2 DYEFYEBERI 11
                                                           3 DYKFYDNKRI 12
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99 KFYDSKRSD 107
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ORGANISM: Zea mays
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  Matches
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Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: INFORMATION:
APPLICANT: APPLICANT: Avoid K.
APPLICANT: Blants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 254882
LENGTH: 70
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                                                                                               CURRENT APPLICATION NUMBER: 05/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PELING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-03-09

PRIOR PILING DATE: 2001-03-09
                          APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: BLITRA.034A
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Pred. No. 60;
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85.7%; Pred. No. 2.9e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: MRT4577_16402C.1.pep
US-10-425-115-254882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: MISC FEATURE
COCATION: (119)...(119)
COTHER INFORMATION: X=any amino acid
US-10-282-122A-73481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Salmonella paratyphi
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
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ORGANISM: Zea mays
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Sequence 42709, Application US/10425114
Fublication No. US2004003488A1
Fublication No. US2004003488A1
GENERAL InvoRMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Edou, Yihua
APPLICANT: Edou, Yihua
APPLICANT: Cacen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)8
CURRENT APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Sequence 62912, Application US/10425114

Publication No. US20040034888A1

Sequence 62912, Application US/2004003488A1

September 1000, Yingdong

September 1000, Yingdong

September 1000, Yingdong

September 1000, You and No.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114
                    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21 (2313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 61683 LENGTH: 131
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                                                                                                                                                                                                                                                                                                                                                                              Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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US-10-425-114-61683
                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 15;
Pred. No. 1.1e+02;
1; Mismatches 1;
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US-10-425-114-42709
                                                                                                                                                                                                                                                                                                                                                                           54.2%;
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Best Local Similarity 77.5-
Local 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays
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US-10-425-114-47855

Sequence 47855, Application US/10425114

Publication No. US200400348881

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Scveen, Scveen E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT PILLING DATE: 2003-04-28
                         APPLICANT: La Rosa, Thomas J.
APPLICANT: Rovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 307333
LENGTH: 115
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Pred. No. 1e+02;
1; Mismatches 1; Indels
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US-10-425-114-47855
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US-10-425-115-307333
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US-10-425-114-61683
US-10-425-114-61683
Sequence 61683, Application US/10425114
Sepuration No. US200400348881
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.2%;
Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.6
From 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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LENGTH: 121
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Query Match
Best Local Similarity
          ORGANISM: Zea mays
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US-10-437-963-104111
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US-10-425-114-72110
Sequence 72110, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 72110
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48114, Application US/10425114

Sequence 48114, Application US/20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Partic OF INVENTION: Nouleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENCE: 38-21(5313)8

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 146
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                                                                                                                                              ; OTHER INFORMATION: Clone ID: LIB3067-050-C2_FLI.pep
US-10-425-114-62912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: LIB36-012-F10_FLI.pep
US-10-425-114-72110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y match 54.2%; Score 39; DB 15; Local Similarity 77.0%; Pred. No. 1.2e+02; les 7; Conservative 1; Mismarchee 1
                                                                                                                                                                                                       Score 39; DB 15;
Pred. No. 1.2e+02;
1; Mismatches 1;
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 62912
LENGTH: 136
                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                           120 KFYDSKRSD 128
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ORGANISM: Zea mays
                                                                                                       ORGANISM: Zea mays
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Best Local S:
Matches 7
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Sequence 104111, Application US/10437963

Sequence 104111, Application US/10437963

Sequence 104111, Application US/10437963

Sequence 104111, Application NS . US/20040123343A1

SEQUENCE 104. US/20040123343A1

SEQUENCE 105. US/20040123343A1

SEQUENCE 105. US/204012

SEQUENCE 105. US/204012

SEQUENCE 105. US/204901

SEQU
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                                                                                                                                                           Length 146;
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                                                                                                                                                                                                                                             1; Indels
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/ OTHER INFORMATION: Clone ID: PAT_MRT4530_101476C.1.pep

US-10-437-963-104111
; FEATURE:
1. OTHER INFORMATION: Clone ID: LIB3150-012-A11_FLI.pep
US-10-7425-114-48114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50, Application US/09893737
Fatent No. US20020110855A1
GENERAL INPORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 2001-06-28
CURRENT FILING DATE: 2001-06-28
FRIOR PRILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOUTHARE: PASELSEQ for Windows Version 3.0
SEQ ID NO 50
LENGTH: 369
                                                                                                                                                       Score 39; DB 15;
Pred. No. 1.3e+02;
1; Mismatches 1
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                                                                                                                                                           Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Matches 7; Conservative
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130 KFYDSKRSD 138
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-09-893-737-50
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: AND MAIN Co. Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Brabazuk, Brad
APPLICANT: Brabazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION WUBBER: US/10/437,963
CURRENT FILING DATE: 2000-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
SEQ ID NO 141960
                                                                                                                                                                                                                    APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA. 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
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PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
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NUMBER OF SEQ ID NOS: 78614
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Pred. No. 8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                    Carr, Grant
Yamamoto, Robert
Forsyth, R.
     alone, Cheryl
aselbeck, Robert
                                                                                      ýskind, Judith
Mall, Daniel
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US-10-282-122A-78226
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PELICATION NUMBER: 06/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELICATION NUMBER: 60/230,365
PRIOR PELICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/257,931
PRIOR PELICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-06
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     Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 74629
LENGTH: 872
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     1; Indels
     1; Mismatches
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Pred. No.
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                             US-10-282-122A-74629
; Sequence 74629, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
Trawick, John
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  7; Conservative
                                                                                                  620 KFYDSKRSD 628
                                                        5 KFYDNKRID 13
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Best Local Similarity
Matches 8; Conserva
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US-10-282-122A-78226
Matches
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Gaps

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3; Indels

us-09-719-379a-3.rapb

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RESULT 33
US-10-424-599-248762
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2000-3-022

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PLILNG DATE: 2000-05-23

PRIOR PLILNG DATE: 2000-05-23

PRIOR PLILNG DATE: 2000-05-26

PRIOR PLILNG DATE: 2000-05-66

PRIOR PLILNG DATE: 2000-01-03

PRIOR PLILNG DATE: 2000-01-03

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-11-27

PRIOR PLILNG DATE: 2000-12-02

PRIOR PLILNG DATE: 2000-12-02

PRIOR PLILNG DATE: 2000-12-02

PRIOR PLILNG DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-03

PRIOR PLING DATE: 2001-02-03

PRIOR PLING DATE: 2001-02-03

PRIOR P
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Pred. No. 2.6e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                     52.8%; Score 38; DB 16; Length 187; 66.7%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                      1; Indels
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_43012C.1.pep
                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51668, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%;
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                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                            176 KYYDNKLLD 184
                                                                                                                                                                                                                                                                                                                                       5 KFYDNKRID 13
                                                                                                                ; OTHER INFORMATION
US-10-437-963-141960
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US-10-282-122A-51668
                                                                                                                                                                                                     Query Match
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us-iv-so-iso-iso-o-base out of the particle of
Sequence 249762, Application US/10424599
Fublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cano Yord K
APPLICANT: Cano Yord Wei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2010-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
NUMBER OF SEQ ID NOS: 285684
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US-10-437-963-193680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , OTHER INFORMATION: Clone ID: PAT_MRT3847_66661C.1.pep
US-10-424-599-248762
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; Sequence 23664, Application US/10369493
; Publication No. US20030233675A1
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Best Local Similarity 77.6
From 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 RGDYDFYEN 76
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APPLICANT: Sivasupramaniam, Sakuntala
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO ANTHONOMUS INSECTS, AND METHODS
TITLE OF INVENTION: OF USE
FILE REFERENCE: 30-21(51932)C
CURRENT APPLICATION NUMBER: US/10/360,899
PRIOR APPLICATION NUMBER: US/20/4,367
PRIOR PELING DATE: 2000-05-15
PRIOR PELING DATE: 2000-05-15
PRIOR PELING DATE: 2000-05-15
PRIOR PELING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Petentin version 3.2
SEQ ID NO 10
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APPLICANT: PADICARU, WIRALIDHARA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-062
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Pred. No. 9.1e+02;
4; Mismatches 3; Indels
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APPLICANT: Roziel, Michael G.
APPLICANT: Buck, Nicholas B.
APPLICANT: Duck, Nicholas B.
APPLICANT: Carr, Brian
TITLE OF INVENTION: AXMI-014, A Delta-Endotoxin Gene and
TITLE OF INVENTION: Methods for Its Use
TITLE OF INVENTION: Methods for Its Use
TITLE OF INVENTION: Methods for Its Use
TILL REPERRNCE: 045600/274143
CURRENT APPLICATION NUMBER: US/10/782,141
FRIOR PILLING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PSESEE for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 14;
Pred. No. 9.1e+02;
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Publication No. US20020192748A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-782-141-19
; Sequence 19, Application US/10782141
; Dublication No. US20040197917A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-360-899-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Bacillus thuringiensis US-10-782-141-19
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Best Local Similarity 41.7
Matches 5; Conservative
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611 KGDYVFYDSRHV 622
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Best Local Similarity 41.7
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-908-193-35
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APPLICANT:
APPLICANT:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B
FILE REFERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23664
LENGTH: 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Monsanto Company
APPLICANT: Monsanto Company
APPLICANT: Fleac, Barbara
APPLICANT: Kleager, Elyaia
APPLICANT: Mettus, Anne-Marie
APPLICANT: Moshiri, Farhad
APPLICANT: Sivasupramaniam, Sakuntala
APPLICANT: Sivasupramaniam, Sakuntala
APPLICANT: Sivasupramaniam, Sakuntala
APPLICANT: Sivasupramaniam, Sakuntala
TITLE OF INVENTION: POLYPEPTIDE COMPOSITIONS TOXIC TO ANTHONOMUS INSECTS, AND METHODS
FILE REFERENCE: 38-21(51932)B
CURRENT APPLICATION NUMBER: 60/204,367
PRIOR APPLICATION NUMBER: 60/204,367
PRIOR PILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 722
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Pred. No. 9e+02;
2; Mismatches 3; Indels
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Pred. No. 9.1e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09853533A Patent No. US20020103362A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/10360899
Publication No. US20030229919A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.8%;
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; ORGANISM: Escherichia coli
US-10-369-493-23664
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Best Local Similarity 41.7
Matches 5; Conservative
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611 KGDYVFYDSRHV 622
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Best Local Similarity 58.3
Matches 7; Conservative
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US-09-853-533A-10
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US-10-360-899-10
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RESULT 40

US.10-369-493-3803

Sequence 3803, Application US/10369493

Sequence 3803, Application US/10369493

Sequence 3803, Application US/10369493

Sublication No. US20030233675A1

Sublication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052) B.

CURRENT APPLICATION NUMBER: US 40/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 3803

LENGTH: 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 9; Length 788; Pred. No. 9.9e+02; 3; Mismatches 3; Indels
CURRENT APPLICATION NUMBER: US/09/908,193
                      CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: 60/220,273
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-27
PRIOR PILING DATE: 2000-07-27
PRIOR PILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/218,970
PRIOR PILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
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; ORGANISM: Neurospora crassa
US-10-369-493-3803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SDYKFYDNKRID 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-908-193-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
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Search completed: November 24, 2004, 10:00:14 Job time : 50.0326 secs

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TYPE: amino acid
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Sequence 10, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 3619, A
Sequence 51536, A
Sequence 1305, Ap
Sequence 1205, Ap
Sequence 1205, Ap
Sequence 1210, A
Sequence 21255, A
Sequence 21258, A
Sequence 21288, A
Sequence 1426, Ap
Sequence 1426, Ap
Sequence 1426, Ap
Sequence 1426, Ap
Sequence 1426, A
                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                             November 24, 2004, 09:14:14; Search time 11.4457 Seconds (without alignments) 75.324 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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                                                                                                                                                                                                                                                                                                          Issued Patents AA:*

(GgDZ 6/ptodata1/iaa/5A_COMB.pep:*
(GgDZ 6/ptodata1/iaa/5B_COMB.pep:*
(GgDZ 6/ptodata1/iaa/6A_COMB.pep:*
(GgDZ 6/ptodata1/iaa/6B_COMB.pep:*
(GgDZ 6/ptodata1/iaa/PCTUS COMB.pep:*
(GgDZ 6/ptodata1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-853-533A-10
US-09-489-039A-13001
US-09-235-451-25
US-09-978-303-25
US-08-633-768A-2
                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                      478139 segs, 66318000 residues
                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                               1 RSDYKFYDNKRID 13
                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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72
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Match Length
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341
388
1131
1221
107
722
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843
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Maximum DB e
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                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                            Database
                                                                Run on:
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Sequence 2, Application US/08457997B

Sequence 2, Application US/08457997B

Patent No. 5766608

GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STREET: Onlo
CITY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/457,997B
FILING DATE:
CLASSIFICATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPRAX: (216) 622-8458
TELEBRAX: (216) 622-8458
TELEBRAX: (216) 221-0816
SOUTHOR FURDAMENTOR:
TELEBRAY: (216) 22-8458
TELEBRAY: (216) 22-8458
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.7%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 359 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.7
Best Local Similarity 77.8
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-457-9978-2
  1 RSDYKFYDN 9
                                      1 RSDYKFYED 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSDYKFYDN 9
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                                                                                                                       US-09-148-711A-10
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          Sequence 1, Application US/09148711A

Patent No. 6436405

Reneral INFORMATION:

APPLICANT: The Ohio State University

TITLE OF INVENTION:

FILE REFERENCE: 18525-04010

CURRENT APPLICATION NUMBER: US/09/148,711A

CURRENT PILING DATE: 1998-09-04

PRIOR PLING DATE: 1998-00-02

NUMBER OF SEQ ID NOS: 125

SOFTWARE: Patentin version 3.0

SEQ ID NO: LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 4; Length 18;
Pred. No. 0.57;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Bakaletz, Lauren O.
APPLICANT: Raumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.7%; Score 43; DB 2; Length 40; 77.8%; Pred. No. 1.3; cive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIABE: OILS.A.

SIATE: U.S.A.

ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/460,502
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING ALLES CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLICK, MARY E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00120
TELECOMMUNICATION INFORMATION:
TELEPAN: (216) 241-0816
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 40 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/08460502
Patent No. 5843464
                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Haemophilus influenza
US-09-148-711A-1
                                                                                                                                                                                                                                                                                                                                                                                          59.78;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RSDYKFYDN 9
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STRANDEDNESS: 817
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US-08-460-502-10
US-09-148-711A-1
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Sequence 10, Application US/09148711A

Sequence 10, Application US/09148711A

Parent No. 6436405

GENERAL INFORMATION:

APPLICANT: The Ohio State University

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/148,711A

CURRENT FILING DATE: 1998-09-04

PRIOR APPLICATION NUMBER: 08/460,502

PRIOR APPLICATION NUMBER: 08/460,502

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.0

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LEMBER OF 10 10

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Pred. No. 1.3;
2; Mismatches 0; Indels
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NGS-0210-394-1
Sequence 1, Application US/08210394
Sequence 1, Application US/08210394
Patent No. 577021
Patent No. 5770213
Patent No. 5770213typable Haemophilus
TITLE OF INVENTION: Influencae PS Protein as a Vaccine for No. 5770213typable
TITLE OF INVENTION: Haemophilus Influencae Strain
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 359;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/451,184
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 4;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24547/04000
TELECOMUNICATION INFORMATION:
TELEPHONE: (216) 622-8416
TELEPHONE: (216) 622-8416
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.78;
                                                                                                                                                                                                                                                                                                                                              : 359 amino acids
amino acid
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TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-451-1184-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 RSDYKFYED 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 07470-8426
                                                                                                                                                                CLASSIFICATION:
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                                                        Gaps
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                59.7%; Score 43; DB 1; Length 359; 77.8%; Pred. No. 13; Live 2; Mismatches 0; Indels
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                                                                                                                                                                                                    Sequence 2, Application US/08467722A
; Sequence 2, Application US/08467722A
; Patent No. 6030626
; GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES: 6
CORRESPONDENCE LABLEES:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Suite 1800 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A>
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/467,722A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-451-184-2

US-09-451-184-2

Sequence 2, Application US/09451184

Settle No. 6562349

GENERAL INFORMATION:

APPLICANT: Kolettukudy, P. E.

TILE OF INVENTION: Obitis Media Vaccine
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: Calfee, Halter and Griswold

STREET: 1400 McDonald Investment Center,

STREET: 800 Superior Avenue

CITY: Cleveland

STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: GOLICK, Mary E
REGISTRATION UNBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 359 amino acids
amino acid
 ; MOLECULE TYPE: protein US-08-467-722A-2
                                                                                                                ||||||||::
138 RSDYKFYED 146
                                                                                       1 RSDYKFYDN 9
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US-08-467-722A-2
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Sequence 440, Application US/09711164
Patent No. 6599738
GENERAL INFORMATION:
APPLICANT: Porsyth, R. Allyn
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Mari
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETY
FILE REFERENCE: ELITRA.008A
CURRENT APPLICATION NUMBER: US 60/164415
FRIOR APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR APPLICATION NUMBER: US 60/164415
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID 0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-00-248-796A-16206

1 Sequence 16206, Application US/09248796A

2 Sequence 16206, Application US/09248796A

3 Patent No. 6747137

4 APPLICATION TO WEINSTON:

5 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANY

7 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

7 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

7 TITLE OF INVENTION: UNMBER: US/09/248,796A

7 CURRENT FILING DATE: 1999-02-13

7 PRIOR PEDLICATION NUMBER: US 60/094,725

7 PRIOR APPLICATION NUMBER: US 60/094,409

7 PRIOR PILING DATE: 1998-08-13

7 PRIOR FILING DATE: 1998-08-13

7 PRIOR PRIOR PRIOR DATE: 1998-08-13

8 PRIOR FILING DATE: 1998-08-13
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Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                   2; Mismatches
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40;
Pred. No.
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                              US/09/328,352
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/32E
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7305
; LEWCTH: 71
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7305
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 55.6%;
Similarity 85.7%;
6; Conservative
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US-09-711-164-440
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16 SSYKFYFNNKIE 27
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Best Local Similarity
Matches 6; Conserv
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US-09-711-164-440
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; Patent No. 6562958
; GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7226-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 36119

LENGTH: 50
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 51536
LENGTH: 50
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                                                       DB 1; Length 338;
19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.9%; Score 41; DB 4; Length 50; 61.5%; Pred. No. 3.6;
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                                                                                                       Indels
                                                       Score 42; DB Pred. No. 19; 1; Mismatches
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                                                                                                                                                                                                                                                                                           US-09-270-767-36319
; Sequence 36319, Application US/09270767
; Patent No. 6703491
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US-09-270-767-51536
Sequence 51536, Application US/09270767
; Patent No. 6703491

; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-51536

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US-09-270-767-36319
                                                       58.3%;
87.5%;
                              Query Match
Best Local Similarity 87.5°
T. Conservative
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RFDHKHYDNDRND 17
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Best Local Similarity 61.5
Matches 8; Conservative
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US-09-328-352-7305
       US-08-210-394-1
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us-09-719-379a-3.rai

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Sequence 21288, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Meinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/248, 796A
CURRENT APPLICATION NUMBER: US 60/074, 725
PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
                                      APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.2%; Score 39; DB 4; I ilarity 75.0%; Pred. No. 2.3e+02; Conservative 1; Mismatches 1:
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...1221
SEQUENCE DESCRIPTION: SEQ ID NO: 3959:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                       STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1221 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3959:
                                                                                                          NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES
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                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
  Patent No. 6583275
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Batent No. 6747137

BACHENT NO. 6747137

BACHATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 19110
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock
TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS
TITLE OF INVENTION: TON 196.132
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
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                        Gaps
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                        1; Indels
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2; Mismatches
  ed. No. 60;
Mismatches
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Best Local Similarity 75.0%; Pred. No. Matches 6; Conservative 1; Mismatc
                                                                                                                                                                       RESULT 14
US-09-248-796A-23255
; Sequence 23255, Application US/09248796A
; Patent No. 6747137
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | |:|:|||
169 DKKYYENKRL 178
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                                                                                          320 FYDNNRVD 327
                                                               6 FYDNKRID 13
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-248-796A-23255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-248-796A-19110
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US-09-107-532A-3959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM:
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APPLICANT: Maier, Henry
APPLICANT: Weier, Henry
APPLICANT: Work, Heidi Jane
APPLICANT: Schnepf, H. Brnest
APPLICANT: No. 5596071e1 Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 715;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,232
FILING DATE:
CLASSIFICATION NUMBER: US/08/158,232
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATPONENTY/AGENT INFORMATION:
AND ATTER APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATPONENTY/AGENT INFORMATION:
AND ATTER APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTONENTY/AGENT INFORMATION:
AND ATTER APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 2; 1
Pred. No. 1.9e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
PPLICATION NUMBER: JP 6/306386
FILING DATE: 09-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: 09LOM, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-856-0PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 413-2200
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 715 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51, Application US/08158232; Patent No. 5596071; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Payne, Jewel
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.3.
7; Conservative
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575 REDPEFYENMRI 586
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                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-08-849-212-6
                                                                                                                                                                                                                                                                                                                                                                              linear
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION UNMER:
US/09/248,796A

CURRENT FILING DATE:
1998-02-13
PRIOR FILING DATE:
1998-08-13
NUMBER:
US/096,409

SEQ ID NOS:
28208

SEQ ID NOS:
28208

SEQ ID NO 14256

LENGTH:
CARRET FOR ALLOW UNMER:
US/09248796A
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US-08-849-212-6

Sequence 6, Application US/08849212

Patent No. 587698

APPLICANT: KIKUCHI, YOSHIMI

APPLICANT: KIKUCHI, TOMOKO

APPLICANT: KOJINA, HIROYUKI

TITLE OF INVENTION: NOVEL LYSINE DECARBOXYLASE GENE AND

TITLE OF INVENTION: NETHOD OF PRODUCING L-LYSINE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: P.C.

ADDRESSEE: P.C.

ADDRESSEE: P.C.

ADDRESSEE: P.C.

ADDRESSEE: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHMAY, SUITE 400

CITY: ARLINGTON

STATE: VA
                                                                                                                                       DB 4; Length 107;
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%; Score 38; DB 4; Length 623; 85.7%; Pred. No. 1.7e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                        0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYER: Floppy disk

CONFUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/08/849,212

FILING DATE: 09-JUN-1997
                                                                                                                                                      Score 38; DB
Pred. No. 26;
4; Mismatches
                                                                                                                                                        52.8%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Candida albicans
US-09-248-796A-14256
                                                         TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                   Query Match 52.8
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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53 FKFYDNQKL 61
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56 SDYKYYD 62
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                                                                                       ; OKGANISM: Candid:
US-09-248-796A-21288
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-248-796A-14256
          ; SEQ ID NO 21288
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APPLICANT: Kennedy, M. Keith
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
APPLICANT: Maier, Henry
APPLICANT: Wick, Heidl Jane
APPLICANT: Olick, Heidl Jane
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Staliward E.
APPLICANT: Schwab, George E.
APPLICANT: George E.
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 52.8%; Score 38; DB 2; Length 722; Best Local Similarity 41.7%; Pred. No. 2e+02; Matches 5; Conservative 4; Mismatches 3; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,891
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PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/158,232
FILING DATE:
APPLICATION NUMBER: 08 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 07/797,645
FILING DATE: 25-MOV-1991
PRIOR APPLICATION DATA:
FILING DATE: 25-MOV-1991
ATTORNERY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6077937
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
      TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                              INFORMATION FOR SEQ ID NO: 51
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acids
STRANDENNESS: single
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611 KGDYVFYDSRHV 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSDYKFYDNKRI 12
                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
                                                                                                                                                                                                                                                                                                                                            US-08-611-928-51
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APPLICANT: Maier, Henry
APPLICANT: Uick, Heidi Jane
APPLICANT: Forcerrada, Luis
APPLICANT: Schwab, George E.
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active
TITLE OF INVENTION: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
OORRESPONDENCE ADDRESS:
ADDRESSE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 1; Length 722;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
COMPUTER: IRM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,928
FILING DATE: 06-MAR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,232
FILING DATE: 24-MAY-1992
CLASSIFICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION: 530
CLASSIFICATION: 530
PRIOR APPLICATION: 530
CLASSIFICATION: NUMBER: US 07/703,977
FILING DATE: 25-MAY-1991
CLASSIFICATION: S30
ATTONNEY/AGENT INPORMATION:
NAME: S311WANCHER: NOWERTION: NUMBER: US 07/703,977
REGISTRATION: NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
      M/SCJ104.C1
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Patent No. 5824792
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kennedy, M. Keith
Randall, John Brooks
Meier, Henry
                                                                                              TELEFAX: 904-372-5800
TELEFAX: 904-372-5800
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acide
TYPE: amino acide
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: peptide
US-08-158-232-51
REFERENCE/DOCKET NUMBER: M.
TELECOMMUNICATION INFORMATION
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : || |||:: :
611 KGDYVFYDSRHV 622
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STATE: FL
COUNTRY: US
ZIP: 32606
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US-09-15.5

US-09-25.451-25

Sequence 25, Application US/09235451

Sequence 25, Application US/09235451

GENERAL INFORMATION:

APPLICANT: Caterina, Michael J.

APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthory J.

TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED

TITLE OF INVENTION: CAPSAICIN RECEPTOR AND USES THEREOF

FILE REFERENCE: 9076/084CIP

CURRENT APPLICATION NUMBER: US/09/235,451

CURRENT FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1997-08-20

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 25

LEMETH: WAREL WAREL WAREL WAS AND WELL WAS AND WE
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APPLICANT: Unlius, David J.

APPLICANT: Caterina, Michael J.

APPLICANT: Caterina, Michael J.

APPLICANT: Brake, Anthony.

TITLE OF INVENTION: Nucleic acid sequences encoding

TITLE OF INVENTION: polypeptides and uses thereof

TITLE OF INVENTION NUMBER: 09/09/978,303

CURRENT PRILING DATE: 1999-01-22

PRIOR PELICATION NUMBER: 60/072,151

PRIOR PELING DATE: 1999-01-22

PRIOR PELING DATE: 1999-08-20

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 25

LENGTH: 843
      Gaps
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      3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.8%; Score 38; DB 4; I
llarity 66.7%; Pred. No. 2.3e+02;
Conservative 2; Mismatches 1;
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 25, Application US/09978303
; Patent No. 6790629
          5,
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600 REDPEFYENMRI 611
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Best Local Similarity 66.7
Matches 6, Conservative
          7; Conservative
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116 FKFYDRRRI 124
                                                                      1 RSDYKFYDNKRI
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: chicken
US-09-235-451-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-978-303-25
          Matches
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APPLICANT: Isaac, Barbara
APPLICANT: Isaac, Barbara
APPLICANT: Isaac, Barbara
APPLICANT: Krieger, Kliger, Blysia
APPLICANT: Moshiri, Farhad
APPLICANT: Moshiri, Farhad
APPLICANT: Sivasupramanian, Sakuntala
APPLICANT: 200.02/04/367
PRIOR APPLICATION NUMBER: 60/204,367
PRIOR PILING DATE: 2000-05-15
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13001, Application US/09489039A

Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GENY Breton et. al
APPLICANT: GENY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13001
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                                                                                                                                                                                                                                                                    Score 38; DB 3; Length 722;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.8%; Score 38; DB 4; Length 722;
41.7%; Pred. No. 2e+02;
tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 4; Length 740;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09853533A Patent No. 6541448 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Klebsiella pneumoniae
US-09-489-039A-13001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.8%;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 722 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-173-891-51
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         : || |||: :
611 KGDYVFYDSRHV 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || |||:: :
611 KGDYVFYDSRHV 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 41.7
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                             1 RSDYKFYDNKRI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RSDYKFYDNKRI 12
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Best Local Similarity
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US-09-489-039A-13001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-853-533A-10
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Gaps
APPLICANT: Nielsen, John
APPLICANT: Marcussen, Jan
APPLICANT: Christensen, Tove
TITLE OF INVENTION: USE OF '-1,4-GLUCAN LYASE FOR PREPARATION OF
TITLE OF INVENTION: 1,5-D-ANHYDROPRUCTOSE
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe "-
STREFF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PURIFIED THERMOSTABLE INORGANIC PYROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS LITORALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ñ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,197
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/633,719
FILING DATE: July 8, 1996
APPLICATION NUMBER: OCT-15-1994
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DYOUS.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.5; DB 4;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                               ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SLANCX, Tricia L.
APPLICANT: SLATKO, Barton E.
APPLICANT: SEARS, Lauren E.
ATILE OF INVENTION: PURIFIED THERMOSTABL
TITLE OF INVENTION: LITORALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-809-267-4; Sequence 4, Application US/08809267; Sequence 4, Application US/08809267; Patent No. 5861296; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2. SEQUENCE CHARACTERISTICS: LENGTH: 1091 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 894 YKFGPDYDTKRLD 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 YKF---YDNKRID 13
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                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                           Sequence 2, Application US/08633768A

Sequence 2, Application US/08633768A

Patent No. 6013504

GENERAL INFORMATION:
APPLICANT: BOJSO, MAJA

APPLICANT: BOJSO, MAJA

APPLICANT: NIELSEN, JAN

TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM

TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSES: Knobbe, Martens, Olson & Bear

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.1%; Score 37.5; DB 3; Length 1091; 61.5%; Pred. No. 3.7e+02; tive 1; Mismatches 1; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYOU7.001APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 92660
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OOPERATING SYSTEM: DOS
SOFTWARE: FastSEN Vereion 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,768A
FILING DATE: 02-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321301.5
FILING DATE: 15-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Altuan, Daniel E
REGISTRATION NUMBER: 34,115
REFREENCE/DOCKET NUMBER: 34,115
REFREENCE/DOCKET NUMBER: DYOUT.001APC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 6632643
GENERAL INFORMATION:
APPLICANT: Yu, Shukun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu, Shukun
Bojsen, Kirsten
Kragh, Karsten
Bojko, Maja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1091 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                894 YKFGPDYDTKRLD 906
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MOLECULE TYPE: protein
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116 FKFYDRRRI 124
                                                                                   4 YKFYDNKRI 12
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: 81
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                           US-08-633-768A-2
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NAME/KEY: UNSURE
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US-09-134-000C-6315
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US-09-134-001C-4547
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GENERAL INFORMATION:
APPLICANT: LENNOX, Tricia L.
APPLICANT: SLATKO, Barton E.
TITLE OF INVENTION:
PURIFIED THERMOSTABLE INORGANIC
TITLE OF INVENTION: PROPHOSPHATASE OBTAINABLE FROM THERMOCOCCUS
TITLE OF INVENTION: LITORALIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STREET: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13662A
FILING DATE:
CLASSIFICATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,267
FILING DATE: 12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                      PILING DATE: 12-MAR-1997
CLASSIFICATION: NUMBER: 05/09/003,207
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13662
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-105-PCT
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION INFORMATION:
TELEPONMUNICATION OF 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,721
FILING DATE: 25-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-105-PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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177 DYKKNENKKVD 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DYKFYDNKRID 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-809-267-4
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Sequence 4547, Application US/09134001C

Sequence 4547, Application US/09134001C

Sequence 4547, Application US/09134001C

Batent NO Sequence 4547, Application US/09134001C

SERVERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT FILING DATE: 1998-08-13

PRIOR PILING DATE: 1997-11-08

PRIOR PLICATION NUMBER: US 60/055,779

PRIOR PILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4547

LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-134-001C-4547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6115.

Sequence 6115.

Sequence 6115.

Betant No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: BNTEROCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: MOMBER: US/09/134,000C

CURRENT PILLING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NOS: 6812

SEQ ID NO 6315
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                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                Length 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 51.4%; Score 37; DB 3; Sest Local Similarity 50.0%; Pred. No. 2.7e+02; Matches 8; Conservative 2; Mismatches 2.
                                                                                                                                                                                                                                                                   Score 37; DB 5;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Enterococcus faecalis
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501 SDYPFYNAQISNKNLD 516
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TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5.
                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                    177 DYKKNENKKVD 187
                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-13662A-4
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                                                                                                                                                                                                                                                                                                   DB 1; Length 123;
66:
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                                                                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ribby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth System of Higher Education
STREET: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,630
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: MONGCO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19122
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                   50.0%; Score 36; 66.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
PCT-US92-10344-10
; Sequence 10, Application PC/TUS9210344
; GENERAL INFORMATION:
TELEFAX: (215) 568-833
TELETAX: (215) 568-833
TELEX: No. 5336667e
INFORMATION FOR EQD ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
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Best Local Similarity 66.7
Matches 6; Conservative
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : | | : | 89 DYKAWDNER 97
                                                                                                                                                                                                                                                                                                                                                                                                              3 DYKFYDNKR 11
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Best Local Similarity
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US-07-893-929A-10
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                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BUCHBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4998
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Pred. No. 63;
                                                  Score 36; DB 4; Length 71;
Pred. No. 37;
                                                                                                              2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Kirby, Edward P.
APPLICANT: Rirby, Edward P.
APPLICANT: Peng, Man-ling
TITLE OF INVENTION: Alboaggregins: Platelet
TITLE OF INVENTION: Agonists Which Bind To Platelet
TITLE OF INVENTION: Membrane Glycoprotein Ib
NUMBER OF SEQUENCES: 10
CORRESPONDER ADDRESS:
ADDRESSEE: Temple University - Of The Common-ADDRESSEE: Temple University - Of The Common-ADDRESSEE: Temple University Services Building
CITY: Philadelphia
STREET: Pointsylvania
COMPURR: Dennsylvania
COMPURR: IBM PS/2
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: Non-DOS
SOFTWARE: Wa-DOS
SOFTWARE: 
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Patent No. 6562958
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US-07-983-929A-10
Sequence 10, Application US/07893929A
; Patent No. 5336667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT CRGANISM: Acinetobacter baumannii US-09-328-352-4998
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803,63
FILING DATE: December 3, 1991
ATTORNEY/AGENT INFORMATION:
                                                  50.0%;
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                            Query Match
Best Local Similarity 66.
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Best Local Similarity 36.4°
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8 KGEYKYFNNKK 18
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US-09-134-000C-6315
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APPLICANT: Tamura, Richard N.
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US
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ANTI-SENSE: NO
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US-09-107-532A-5102
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                                                                                                                                                                      STATE: C. COUNTRY:
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amino acid sequence predicted from the product
which results from amplification of the mouse
ALPHA 3B cDNA with primers 2032/2033."
                                                                                     APPLICANT: Tamura, Richard N.
APPLICANT: Tamura, Richard N.
APPLICANT: Quaranta, Vito
APPLICANT: Quaranta, Vito
TITLE OF INVENTION: INTEGRIN ALPHA SUBUNIT CYTOPLASMIC
TITLE OF INVENTION: DOMAIN POLYPEPTIDES, ANTIBODIES AND METHODS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Thomas Fitting
STREET: 11300 Sorrento Valley Road, Suite 200
CITY: San Diego
STATE: California
COUNTRY: United States
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CDFFK begins at amino acid position 108.
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Pred. No. 83;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                     COMPUTER REALSHELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/695,564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCR0377P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19910603
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR03
TELECOMMUICATION INFORMATION:
TELECHONE: 619-546-1555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: MINO ACID
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US-08-241-387-9
Sequence 9, Application US/08241387
Patent No. 5589570
GENERAL INFORMATION:
                                                     ; Sequence 9, Application US/07695564
; Patent No. 5310874
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Best Local Similarity 54.5-
Best Conservative
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FRAGMENT TYPE: internal
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES
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33 DYKDFDRVRVD 43
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OTHER INFORMATION:

US-07-695-564-9
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LOCATION: 1..153
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
PEATURE:
NAME/KEY: Domain
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               RESULT 36
US-07-695-564-9
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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APPLICANT: Quaranta, Vito
TITLE OF INVENTION: INTEGRIN ALPHA SUBUNIT CYTOPLASMIC
TITLE OF INVENTION: DOMAIN POLYPEPTIDES, ANTIBODIES AND METHODS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: The Scripps Research Institute
STREET: 10666 No. 5589570th Torrey Pines Road, TPC-8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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CDFFK begins at amino acid position 108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 36; DB 1; Length 153;
                                                                                                                                                                                                                                                                  COMPUTER EAADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,387
FILING DATE: 10-MAY-1994
ATTORNEY/AGENT INPORMATION:
APPLICATION NUMBER: US/095,564
ATTORNEY/AGENT INPORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: TSRI241.0D1
TELEPHONE: 619-554-2937
ITELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 153 aniio acids
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 83;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.55,
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DYKFYDNKRID 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Region
LOCATION: 1..153
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 108..112
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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LOCATION: 108.11
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Meaure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomann, Elaine
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

ELING DATE: 18-MAY 1994

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/08/245,511

FILING DATE: 01-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: 20cker NUMBER: 26,742

REGISTRATION INFORMATION:

TELECOMMUNICATION:

TELECOMMUNICATION:

TELEPHONE: 201487.5800
                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08245511
Patent No. 5928900
GENERAL INFORMATION:
                                       NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: P-41,17;
REGISTRATION NUMBER: P-41,17;
REBERCOMMUNICATION INFORMATION:
TELEPHONE: 302-92-4926
TELEPHONE: 302-92-4926
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                50.0%;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.00,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| || |||
76 RESFKIYDIVRID 88
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide US-08-838-543-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
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62.5%; Pred. No. 1.40+02;
tive 3; Mismatches 0; Indels
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US-08-838-543-5
iSequence 5, Application US/08838543
; Patent No. 5994623
; GENERAL INFORMATION:
APPLICANT: REBBERS, ENNO
APPLICANT: BROGLIE, KAREN E.
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE: E. I. DUPONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAMARE
COUNTRY: UNITED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCHIBLE
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
                CITY: Waltham
STATE: Wasachusetts
COUNTR: USA
ZIP: 02354
COMPUTER: EORM: .
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
CORPATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: misc feature
) LOCATION: (B) LÖCATION 1...246
) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:
US-09-107-532A-5102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/838,543
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 246 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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Best Local Similarity
Matches 5; Conserva
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	Indels
+02;	., H
Pred. No. 1.8e+02	Mismatches
45.58;	ative
Similarity	5; Conservative
ca]	Matches

Best Loca. Matches	Best Local Similarity 45.5%; Matches 5; Conservative	<pre>%; Pred. No. 1.8e+02; 5; Mismatches 1; Ir</pre>
ζō	3 DYKFYDNKRID 13	
qa	43 DHRFFDHRGID 53	

Search completed: November 24, 2004, 09:31:40 Job time : 12.4457 secs

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; Search time 59.7717 Seconds (without alignments)
125.141 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                          1825181
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     1825181 seqs, 575374646 residues
                                                                                                           November 24, 2004, 09:11:04
                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                       1 RSDYKFYDNKRID 13
                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                  US-09-719-379A-3
72
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                                                                                                                                                                                    Title:
Perfect score:
                                                                      OM protein
                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Database

066w23 Kluyvenyc 062x56 oryza sativ 063ub7 pasteurella 1938.68 haemophilus 1945.96 haemophilus 1945.96 haemophilus 1945.96 haemophilus 1945.96 haemophilus 1945.96 gamma-pro 196x.93 gamma-pro 196x.93 gamma-pro 196x.93 gamma-pro 196x.93 gamma-pro 196x.93 gamma-pro 196x.93 gamma-pro 196x.19 plasmodium 196x.19 plasmodium 196x.19 plasmodium 199x.19 bordetella 197x.19 bordetella 197x.19 bordetella 197x.19 bordetella 197x.19 bordetella 197x.19 bordetella 198x.19 mycoplasma Q7rkvl plasmodium O86254 haemophilus Description SUMMARIES Q7RQI4 HGP1_HAEIN Query Match Length DB Score Result Š.

ה:פ ממממאלר הממממ		· · 0	
Q9x442 haemophilus Q9xiv1 haemophilus Q4436 haemophilus Q8495 hardyrhizob Q6zew6 synechocyst Bad1784 synechocy G6gub8 pasteurella Q6gub9 pasteurella Q6gub9 pasteurella Q6mu1 pasteurella Q6mu2 pasteurella Q6mu2 pasteurella Q6mu1 pasteurella Q6mu2 mycoplasma Cae76779 mycoplasma Q22067 caenorhabdi	Plasmodium. Plasmodium. J.D., Koo H.L., (Bldwell S.L., Cummings L.M., Cummings L.M., K., Harris M.A., S., Harris M.A., white O.R., S.L., Gardner M.J., model rodent malaria from an entry which is	Length 1047; ; Indels 0; Gaps	
HGPC HAEIN HGBB_HAEIN HGBB_HAEIN HGP3 HAEIN QB 2T91 QB 2EW6 BAD01784 QG GUB8 QG GUB5 QG GUB5 QG GUB5 QG GW1 QB AM1 QB AM2K4 QG MU35 CAE76779	uence update) otation updat semosporida; E., Kooij T.W. E., Selengut Shoaibi A., D., Sinden R. an L. W., Vold an L. W., Vold an L. W., Vold an L. W., Hoffman lysis of the is derived f hotgun (WGS)	Score 51; DB 2; Lengt Pred. No. 5.9; 1; Mismatches 3; In	PRT; 360 AA. Created) Last sequence update)
	26, 26, 26, 26, 11, 11, 11, 11, 11, 11, 11, 11, 11, 1		08, 08,
9.00 1006 4 1006	ULT 1 OTRKV1	70. 69. vative KRID 1 : 4	PRELIMINARY; (TrEMBLrel. (TrEMBLrel.)
	PRELII 04 (TrEM 04 (TrEM 04 (TrEM 04 (TrEM 05 (TrEM 05 (TrEM 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1799; 1790;	Con Con VKF	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	UT 1 Q7RKV1 Q7RKV1 Q7RKV1 O1-MAR-2004 (TEEMBLEEL. O1-MAR-2004 (TEEMBLEEL. ULAMR-2004 (TEEMBLEEL. ULAMR-2004 (TEEMBLEEL. ULAMR-2004 (TEEMBLEEL. ULAMR-2004 (TEEMBLEEL. ULAMR-2004 (TEEMBLEEL. ULAMR-2004 (TEEMBLEEL. NAB-2004 (TEEMBLEEL. AND NAB-2004 (TEEMBLEEL. AND NAB-2004 (TEEMBLEEL. NAB-2004 NA	atch cal S g	LT 2 54 O86254 O86254; 01-NOV-1998 01-NOV-1998
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	SOUR BRADE	S S S	RESULT 086254 ID OO AC OO DT 00

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Bouchier C., Caudron B., Scarpe
Wincker P., Souciet J.L.;
"Genome evolution in yeasts.";
                                                                                                                                                                                                                                                        1 RSDYKFYDNKRID 13
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19 RSTFLFYDNKOLE 31
                                                                                                                                                                                         Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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47 RSSFKFYDRKAV 58
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSDYKFYDNKRI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                              Nature 430:35-44 (2004)
                                                                             SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B1142B04.6.
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BAD10106;
                                                                                                                                                             SEQUENCE
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Q625F0;
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                                                                                                                                                     MEDLINE=9901716; PubMed=9864189;
MEDLINE=9901716; PubMed=9864189;
Tousect N., Rosenau A., Sizaret P.Y., Quentin R.;
Muclectide sequences of genes coding for fimbrial proteins in a rivelectic sequences of genes coding for fimbrial proteins in a cryptic genospecies of Haemophilus spp. isolated from neonatal and refrections.";
Thecr. Immun. 67:8-15(1999).
Thefer. Immun. 67:8-15(1999).
Thecr. Immun. 67:8-15(1999).
Thecr. Immun. 67:8-15(1999).
Thecr. Immun. 67:8-15(1999).
Thecr. Integral to membrane; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
MICATAC: IPRO06664; Bac OmpA.
InterPro; IPR006650; OmpA.LIKE.
MICATAC: IPR006690; OmpA.LIKE.
MICATAC: IPR00691; OmpA.LIKE.
MICATAC: MARCOMAIN.
PRINTS; PR01021; OMPA.COMAIN.
PRINTS; PR01021; OWPAMEANEA.
MINTS; PR01022; OUTRAMBRANEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla B., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicolski M., Oztas S., Ozier-Kalogeropoulos O., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Swennene D., Tekala F., Wasolowski-Louvel M., Westhoff E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.9%; Score 46; DB 2; Length 360; 100.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 AA; 38415 MW; A3209155051CDD69 CRC64;
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Outer membrane protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORFNames=KLLA0B00363g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 RSDYKFYD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSDYKFYD 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                            FROM N.A.
                                            Haemophilus sp.
                                                                                              NCBI_TaxID=740;
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SEQUENCE
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Matches
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Q6CWZ3
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Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein B1142B04.6.
Name=B1142B04.6;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzaee; Oryza.
Nill_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza, Oryza sativa.
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Sasaki I., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
                                                                                                                                                                                                                                                                                                              Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 76;
                                                                                                                                                                               Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382122; CAH01939.1; -.
                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone:B1142B04.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., Katayose Y.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005148; BAD10106.1; -
                                                                                                                                                                                                                                         2122; CAH01939.1; -.
212 AA; 24162 MW; B3888750EF4D6C10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 76 AA; 9017 MW; 91B11512447964F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2004 (TrEMBLrel. 27, Created)
C-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein B1142804.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 2;
Pred. No. 8.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                   .;
7
                                                                                                                                                                                                                                                                                                              Score 44; DB 2
Pred. No. 18;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.7%;
                                                                                                                                                                                                                                                                                                              61.1%;
53.8%;
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Fransmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P45996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
OM53_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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      SO THE FEFF THE SO THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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STRAIN=1613 / Serotype B;
MEDLINE=93366472; Pubmed=8359929;
Munson R.S. Jr., Grass S., West R.;
"Molecular cloning and sequence of the gene for outer membrane protein
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%; Score 43; DB 2; Length 351; 61.5%; Pred. No. 45; ive 1; Mismatches 4; Indels
                                                                                                                    Score 43; DB 2; Length 76;
Pred. No. 8.9;
                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akridge H., Confer A.W., Dabo S.M.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: Belongs to the ompA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 AA; 37694 MW; BCD8F861104354C1 CRC64;
                                                          76 AA; 9017 MW; 91B11512447964F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
04-04 membrane protein P5 precursor (OMP P5).
Name=ompA; Synonyms=ompP5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 AA
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                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006664; Bac_OmpA.
InterPro; IPR006664; OmpA.
InterPro; IPR006665; OmpA/MotB.
InterPro; IPR00690; OMPA_LIKE.
InterPro; IPR000498; OmpA_LIKE.
Pfam; PR00691; OmpA; I.
PRIMTS; PR01021; OMFAMDRAIN.
PRINTS; PR01021; OMFAMDRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000930; OmpA/MotB; 1.
PROSITE; PS01068; OMPA; 1.
SEQUENCE 351 AA; 37694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY643795; AAT57677.1; -
                                                                                                                    58.3%;
EMBL; AP005148; BAD10106.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 RSDYKVYDKEPAD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSDYKFYDNKRID 13
                                                                                                                                               Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 61.5 Matches 8; Conservative
                                                                                                                                                                                                                                                                          47 RSSFKFYDRKAV 58
                                                                                                                                                                                                                                        1 RSDYKFYDNKRI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae
                              Hypothetical protein. SEQUENCE 76 AA; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=95120769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=747;
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P38368;
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6GUB7;
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AC 0M52 H
AC 01-0CT-1
DT 01-0CT-1
DT 01-0CT-1
DE 00-1Ut-1
CON Name=or
CON NCBI_TR
RN [1]
RN [1]
RN [1]
RN RN H
RN H
RN MEDLINI
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Q6GUB7
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STRAIN=NTH1 1128;
MEDLINE=94222555; PubMed=7909539;
Sirakova T., Kolattukudy P.E., Murwin D., Billy J., Leake E., Lim D., Demaria T., Bakaletz L.;
"Role of fimbriae expressed by nontypeable Haemophilus influenzae in pathogenesis of and protection against otitis media and relatedness of the fimbrin subunit to outer membrane protein A.";
Infect. Immun. 62.2002-2020(1994).
--- FUNCTION: Acts as a fimbriae subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
P5 of Haemophilus influenzae.";
Infect. Immun. 61:4017-4020(1993).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-!- SIMILARITY: Belongs to the ompA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-i- SIMILARITY: Belongs to the ompA family.
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Pasteurellaceae, Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.7%; Score 43; DB 1; Length 353; 77.8%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct protein sequencing; Outer membrane; Porin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Outer membrane protein P5 precursor (OMP P5) (Fimbrin).
Name=ompA; Synonyms=ompP5;
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane protein P5
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By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPROOG556; OmpA.
InterPro; IPROOG665; OmpA/MocB.
InterPro; IPROOG690; OMPA_LIKE.
InterPro; IPROOG99; OmpA_tmem.
Pfam; PPO01389; OmpA; 1.
Pfam; PPO01389; OmpA, membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1021; OMPADOMAIN.
ProDom; PD000930; OmpA/MotB; 1.
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006664; Bac_OmpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 AA; 37594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L20309; AAA03346.1; -. HSSP; P02934; 1QJP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 77.8
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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338
316
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Gamma-proteobacterium Hot 75m4.
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Best Local Similarity
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AAP49314;
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Qexess;
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Aguc.
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AAP4

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D AAP4

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                                                                                                                                              HSSP; P02934; 1BXW.
R InterPro; IPR006664; Bac_OmpA.
R InterPro; IPR006669; OmpA.
R InterPro; IPR006690; OmpA.
R InterPro; IPR006690; OmpA_LIKE.
R InterPro; IPR006690; OmpA_LIKE.
R InterPro; IPR00691; OmpA_Like.
R Pfam; PF00691; OmpA, membrane; 1.
R Pfam; PF001389; OmpA membrane; 1.
R PRINTS; PR01021; OMPANOMAIN.
R PROSITE; PS01068; OmpA/MottB; 1.
R PROSITE; PS01068; OmpA/MottB; Fimbria; Outer membrane; Porin; Signal; Transmembrane.
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EMBL; AY236223; AAP70366.1; - . SECEB2949EB94AE4 CRC64; SEQUENCE 404 AA; 46151 WW; SECEB2949EB94AE4 CRC64;
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BEDLINE-22894188; PubMed=14532085;
Voget S., Leggewie C., Uesbeck A., Raasch C., Jaeger K.E., Streit W.R.;
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By similarity.
OmpA-like.
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or send an email to license@isb-sib.ch).
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NCBI_TaxID=77133;
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05-JUL-2004 (TEMBLrel. 27,
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Matches 8, Conservative
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76 TDPKFYNNKRI 86
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MEDLINE-22894188; PubMed=14532085;
Voget S., Leggewie C., Uesbeck A., Raasch C., Jaeger K.E.,
Voget S., Leggewie C., Uesbeck A., Rasch C., Jaeger K.E.,
Voget S., Englewie C., Uespecking for novel biocatalysts in a soil metagenome.";
Appl. Environ. Microbiol. 69:6235-6242(2003).
EMBL; AY212800; AAP70389.1; -.
EMBL; AY212800; AAP49314.1; -.
SRQUENCE 451 AA; 51461 MW; DE9CE0C8628521E9 CRC64;
                                                                                                                                                          "Prospecting for Novel Biocatalysts in a Soil Metagenome."; Pappl. Environ. Microbiol. 69:6235-6242 (2003).
EMBL, AY236223; AAP70366.1; -
SEQUENCE 404 AA3, 46151 MW; SRCEB2949EB94AE4 CRC64;
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Appl. Environ. Microbiol. 69:6235-6242(2003).
EMBL; AY212800; AAP49314.1; -.
SEQUENCE 451 AA; 51461 MW; DE9CE0C8628521E9 CRC64;
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SEGUENCE FROM N.A.
Voget S., Leggewie C., Uesbeck A., Raasch C., Jaeger K.E.,
Streit W.R.;
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Streit W.R.;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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uncultured bacterium.
Bacteria; environmental samples.
Bacteria, environmental samples.
NCBI_TaxID=77133;
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NCBI_TaxID=77133;
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123 TDPKFYNNKRI 133
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76 TDPKFYNNKRI 86
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Complete proteome, Hypothetical protein, Signal. SIGNAL 1 16 Potential.
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SEQUENCE FROM N.A.
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QBIIG1;
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteuralla multocida Pm70.";
Proc. Natl. Acad. Sci. U.S. A. 98:3460-3455(2001).
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Pasteurellaceae; Pasteurella.
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Streit W.R.;

"Prospecting for Novel Biocatalysts in a Soil Metagenome.";

Appl. Environ. Microbiol. 69:6235-6242(2003).

EMBL; AX236225, AAP70389.1; -.

SEQUENCE 451 AA, 51461 MW; DE9CEOC8628521E9 CRC64;
                     Score 43; DB 2; Length 451;
Pred. No. 59;
2; Mismatches 1; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Hypothetical UPF0192 protein PM0659 precursor orderedLocusNames=PM0659;
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NCBI_TaxID=77133;
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123 TDPKFYNNKRI 133
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17 1905 Hypothetical UPF0192 protein PM0659.
1905 AA; 214427 MW; PED71CE8D61F7C78 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical prolipoprotein.
05-GLOGUSANDASS-MSC 0927;
Mycoplasma mycoides (Subsp. mycoides SC).
Bacteria; Pirmicutes; Mollicutes; Mycoplasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                           59.7%; Score 43; DB 1; Length 1905; 60.0%; Pred. No. 2.7e+02; tive 4; Mismatches 0; Indels
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Pred. No. 3.96+02;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
ORFNames=PPII 0213;
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2616 AA.
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PROSITE; P800030; RRM RNP_1; UNKNOWN_1.
Hypothetical protein. 313007 MW; C8934D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE014839; AAN35797.1; -.
InterPro; IPR011591; Botulinum.
InterPro; IPR000717; PCI.
InterPro; IPR00504; RNA_rec_mot.
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1933 EYKFYDNENKD 1943
                                                                                                                                         Local Similarity 60.0
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NCBI_TaxID=2287;
                                                                                            falciparum.
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Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
                     Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlan M.; "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGII, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                             Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGIT, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                              Gaps
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Mycoplasma mycoides (subsp. mycoides SC).
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
07FNAmnes-PPI0 0028;
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                     Score 42, DB 2; Length 124;
Pred. No. 22;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 2; Length 124;
Pred. No. 22;
2; Mismatches 3; Indels
                                                               (CBPP).";
Genome Res. 14:221-227(2004).
EMBL: BX42645; CAE7757.11,-
Complete Protecome; Hypothetical protein; Lipoprotein.
SEQUENCE 124 AA; 14612 MW; 5845D717CA3070CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BX842645; CAE77537.1; -.
Hypothetical protein; Lipoprotein.
SEQUENCE 124 AA; 14612 MW; 5B45D717CA3070CA CRC64;
                                                                                                                                                                                                                                                                                      (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                 124 AA.
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                                                                                                                                      58.3%;
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                                                                                                                                  Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 58.3
7; Conservative
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                                                                                                                                                                                  1 RSDYKFYDNKRI 12
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        PubMed=14762060;
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PubMed=14762060;
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QBIK12,
01-MAR-2003 (
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02-MAR-2004
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 STRAIN=PG1
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CAE77537;
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081K12
AC 081K1.
AC 081K1.
DT 01-MAD
DT 01-MAD
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GN ORENWA
OC BUKAT
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STRAIRSATCC 35092 / DSM 1617 / P2;

STRAIRSATCC 35092 / DSM 1617 / P2;

STRAIRSATCC 35092 / DSM 1617 / P2;

She Qi, Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

De Moors A., Erauso G., Fletcher C., Kozdon P.M.K.,

Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";

Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
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Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S., Nnee V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengt J., Haft D., Mather M.W., Vaidya A.B., Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Worfedden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., "Genome sequence of the human malaria parasite Plassmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein ORF-c22_006 (Hypothetical protein SS00545).
Hypothetical protein ORF-c22_006 (Hypothetical protein SS00545).
Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
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Hypothetical protein.
SEQUENCE 248 AA; 30051 MW; 2120EC2D2E14A68B CRC64;
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SEQUENCE 286 AA; 32864 MW; 8C478AF9A48D4AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 2;
Pred. No. 47;
3; Mismatches
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Pfam; PP00076; RRM 1; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                          Nature 419:498-511(2002).
EMBL; AE014829; AAN35226.1; -.
HSSP; P09651; 1HA1.
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53.8%;
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Query Match
Best Local Similarity 53.00.
Best Local Similarity 53.00.
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172 RNDYRNYDRRSID 184
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Complete proteome
SEQUENCE 870 AA
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-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R., III, Raine J.D., Sinden R.E., Harris M.A., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Carlocci D.J., Vetler J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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Name=PY01693;
Plasmodium yoelli yoelli.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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Bacteroides thetaiotaemicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                               DB 2; Length 286;
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                                                                                           3; Indels
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EMBL, AABLO1000456; EAA21053.1; -.
InterPro, IRR006477; Nir. bir. cir.
Pfam; PF06022; Cir Bir Yir, I.
TIGRFAMS; TIGR01590; yIr-bir-cir Pla; 1.
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Last annotation update)
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                                                                                     3; Mismatches
                               Score 42;
Pred. No.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last secon
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STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
                               58.3%;
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Query Match
Best Local Similarity 53.8'
7; Conservative
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53 KSYYNFYDSSKID 65
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Best Local Similarity 58.3
7; Conservative
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OTRNXO
DT OOTRNX
AC OTRNX
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084446
AC 084441
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DT 01-JU
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DE Putat
GN Dreat
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Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K., Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetalotaomicron symbiosis.";
Science 299:2074-2076 (2003).
EMBL, ARO16936, AA07730.1;
InterPro; IPR005198; Glyco_hydro_76.
InterPro; IPR005198; Glyco_hydro_76.
InterPro; IPR068928; Glyco_hydro_76; I.
Complete proteome.
SEQUENCE 517 AA; 59079 MW; 87D3392046B0592A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=TOhama I / ATCC BAA-589 / NCTC 13251;
MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
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Last annotation update)
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Pred. No. 1e+02;
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EMBL; BX640416; CAE42047.1; -.
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01-0CT-2003 (TrEMBLrel. 25, L
01-MAR-2004 (TrEMBLrel. 26, L
Putative exported protein.
OrderediscusNames=BPP1991;
Bordetella parapertussis.
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Best Local Similarity 58.3%;
Matches 7; Conservative
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RADYVYYNGKRI 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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66.78;
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OrderedLocusNames=BT3024;
731 RADYVYYNGKRI 742
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                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                  Caulobacter crescentus
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Best Local Similarity
8; Conserve
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                                                                                                                                                                                                                                                                                                             NCBI TaxID=155892;
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01-JUN-2001
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                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=12822 / ATCC BAA-587;

X MEDLINE=282295954; PubMed=12910271; DOI=10.1038/ng1227;

X Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bantley S.D., Mungall K.L.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Chervach I.,

RA Achtman T., Collins M., Cronin A., Davis P., Doggett J.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Unit L., Whitehead S., Barrell B.G., Maskell D.J.;

R Gomparative analysis of the genome sequences of Bordetella pertussis,

RT Gomparative analysis and Bordetella bronchiseptica.";

RE Nat. Genet. 35:32-40(2003).

RE M. SERIE, BKAG4029; CAE37291.1; -.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE CARAINERSO / ATCC BAA-588;

NA PARKAIN-RSD OF THE CARAINERSO / ATCC BAA-588;

NA PARKAIN J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

NA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

NA Achtman M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Arkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Relivell T., Goble A., Hamilan N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Gromparative analysis of the genome sequences of Bordetella pertussis,

Not Constant S., Norberczak Barrell B.G., Maskell D.J.;

Hordetella parapertussis of the genome sequences of Bordetella pertussis,

Not Constant S., Norberczak B., Comparative analysis of the genome sequences of Bordetella pertussis,

Norberczak B., Comparative analysis of the genome sequences of Bordetella pertussis,

Norberczak B., Comparative analysis of the genome sequences of Bordetella pertussis,

Norberczak B., Comparative A., Comparat
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  Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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Pred. No. 1.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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Last annotation update)
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EMBL; BX640443; CAE32675.1; -.
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                   Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
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731 RADYVYYNGKRI 742
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
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STRAIN=ATCC 19089 / CB15;

MEDILINE=21134509; PubMed=11259647; DOI=10.1073/pnas.061029298;

MISTINE=21134509; PubMed=11259647; DOI=10.1073/pnas.061029298;

Misting M.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Reclonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,

Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,

Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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TIGREAMs; TIGRO1782; TonB-Xanth-Caul; 1.
Complete proteome; Membrane; Outer membrane; Receptor; TonB box.
SEQUENCE 903 AA; 99453 MW; 888933577283E7C9 CRC64;
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Caulobacteraceae; Caulobacter.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative outer membrane protein, probably involved in nutrient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteroides thetaiotaomicron.
Bacteria, Bacteroidetes, Bacteroides, Bacteroidaceae, Bacteroides.
Bacteroidaceae, Bacteroides.
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STRAIN-BYNE-15482 / ATCC 29148;
MEDLINE-2255068; Pubmed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- SUBCELLUIAR LOCATION: Outer membrane (By similarity).
EMBL; AE006777; AAKZ2979.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                   01.-UUN-2001 (TrEMBLrel. 17, Last sequence update)
1-UNAR-2004 (TrEMBLrel. 26, Last annotation update)
Tonb-dependent receptor, putative.
OrderedLocusNames=CC0995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 2; I Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0019867; C:outer membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000512; F:transporter activity; IEA.
InterPro; IPR001031; TonB receptor.
InterPro; IPR010104; TonB receptor.
  903 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1021 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last anno
                                                        (TrEMBLrel. 17, Created)
PRT;
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Isomerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Q6МТВ3
С6МТВ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CBPP) . .
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                Chiang H.C., Hooper L.V., Gordon J.I., "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.;

"Integrated mapping, chromosomal sequencing and sequence analysis of Cryptosporidium parvum.";

Genome Res. 0:0-0(2003).

EMBL; BX538352; CAD98428.1; --.

EMBL; BX538352; CAD98428.1; --.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008026; F:ATP binding; IEA.

GO; GO:0008026; F:ATP binding; IEA.

GO; GO:0008026; F:ATP binding; IEA.
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                                                                                        EMBL; AED16312. ACOUNT COLUCE membrane (By similarity).

EMBL; AED16318, AAO78130.1; -

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006810; P:transporter activity; IEA.

GO; GO:0006810; P:transporter activity; IEA.

GO; GO:0006810; P:transporter activity; IEA.

InterPro; IPR008969; Carboxypepp reg.

InterPro; IPR00531; TonB receptor.

Effan; PF00593; TonB dep_Rec; I.

Complete protecome; Membrane; Outer membrane; Receptor; TonB box.

SEQUENCE 1021 AA; 112777 MW; 9E80FA41FBF59FEF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Alveolata; Apicomplexa, Coccidia, Eimeriida;
Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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InterPro; IPR001464; DEAH box.
InterPro; IPR001650; Helicase C.
InterPro; IPR001005; Myb DNA Dinding.
InterPro; IPR000330; SNFZ N.
Pfam; PF00271; Helicase C; I.
Pfam; PF00176; SNFZ N; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                           Science 299:2074-2076(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNF2 helicase, possible. ORFNames=1MB.528;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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341 KSDYSFFDNR 350
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SMART; SM00490; HELICC;
SMART; SM00717; SANT; 2.
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820 DWQFYDKKRI 829
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Matches 7; Conserv
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AC 07YYQ2
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RESULT 28

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                                                                                                                                                                                                                                                                                                                                                              Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGIT, the causative agent of contagious bovine pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type strain PGIT, the causative agent of contagious bovine pleuropneumonia
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Bacteria, Firmicutes; Mollicutes; Mycoplasmataceae; Мусорlавma.
NCBI TaxID=44101;
                                              05-JTU-2004 (TrEMBLrel. 27, Created)
05-JTU-2004 (TrEMBLrel. 27, Last sequence update)
05-JTU-2004 (TrEMBLrel. 27, Last sequence update)
05-JTU-2004 (TrEMBLrel. 27, Last annotation update)
Mannose-6-phosphate isomerase (EC 5.3.1.8).
Mamespmi; OrderedLocusNames=MSC 0495;
Mycoplasma mycoides (subsp. mycles SC).
Bacteria; Firmicutes; Mollicutes; Mycoplasma.
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EMBL; BX642643; CAE77123.1; -.

EMBL; BX642643; CAE77123.1; -.

GO; GO:0016476; F: Hsomerses activity; IEA.

GO; GO:0004476; F: Hannose-6-phosphate isomerase activity; IEA.

InterPro; IPR011051; RmlC like_cupin.

Pfam; PF01238; PML_type1; 1.

Complete proceome; Isomerase.

SEQUENCE 309 AA; 35928 MW; 0508225F88197B12 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
13-APR-2004 (TrEMBLrel. 27, Last annotation update)
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309 AA
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PMI OR MSC_0495.
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  PRT;
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EMBL; BX842643; CAE77123.1; -.
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Matches 7; Conservative
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PRELIMINARY;
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189 YRFYDYNRID 198
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Best Local Similarity
7, Conserve
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=44101;
                                                                                                                                                                                                                                                                                                                  STRAIN=PG1;
PubMed=14762060;
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PubMed=14762060;
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"Whole-genome random sequencing and assembly of Haemophilus influenzae
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SEQUENCE
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REPEAT
SITE
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REPEAT
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                                                                                                                                                                                                                                                                                                                     "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii,";
Nature 419:512-519(2002).

-1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MELSINE=95350630; PubMed=7542800;
Rerlachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G.G., FitzHugh W., Fields C.A., Gocayne J.D., Weidman J.F., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                           STRAIN=17XNL;
PubMed=1236865;
PubMed=1236865;
Silva J.C., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M.,
Silva J.C., Exnolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable hemoglobin and hemoglobin-haptoglobin binding protein 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                    Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                             56.9%; Score 41; DB 2; Length 354; 87.5%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 354 AA; 41675 MW; 700A43802C5EA7F1 CRC64;
                                                                     Last sequence update)
Last annotation update)
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16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
                                   354 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                           Created)
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                 preliminary data.
EMBL; AABL01000295; EAA20366.1; -.
                                                      01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor.
OrderedLocusNames=HI0635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 KFYDNKKI 230
                                                                                            Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KFYDNKRI 12
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=73239;
                                                                                                         Name=PY01113;
                                                                                                                                                                                                                                                                                                               Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAEIN
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P44795;
                                  Q7RQ14
           RESULT 30
Q7RQ14
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                                                                                                                                                                                                                                                                                Pfam; PF04886; PT; 1.
Pfam; PF04886; PT; 1.
TIGRRAMS; TIGR01785; TonB-hemin; 1.
TIGRRAMS; TIGR01786; TonB-hemiactrns; 1.
PROSITE; PS00430; TONB DEPENDENT REC 1; FALSE NEG.
PROSITE; PS01156; TONB DEPENDENT REC 2; 1.
Complete proteome; Multigene family; Outer membrane; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                          IDENTIFICATION BY MASS SPECTROMETRY.
MEDLINE=20137488; PubMed=10675023;
Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probable hemoglobin and hemoglobin-haptoglobin binding protein 1.
7 X 4 AA tandem repeats of Q-P-T-N.
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TonB C-terminal box.
MW; 370CB515523F2788 CRC64;
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InterPro; IPR010916; TONB BOX N.
InterPro; IPR010949; TONB_hemlactrns.
InterPro; IPR010931; TONB_receptor.
InterPro; IPR010917; TONB_recept_C.
                                                                                                                                                                                                                                             Coudert B.;
Unpublished observations (AUG-2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U32746; AAC22294.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; TonB box; Transport.
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Science 269:496-512(1995).
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nes 7; Conservative
                                                                                                                                                                                                                         CONCEPTUAL TRANSLATION.
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REPEAT
REPEAT
SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Outer membrane.

MISCELLANEOUS: This protein is subject to phase-variable expression associated with alteration in the length of the CCDA repeat region. This mechanism is called slipped-strand mispairing. Addition or loss of CCDA repeat units would change the reading frame and result in introduction of stop codons downstream of the repeat region. This may be a mechanism of regulation and a way to avoid the immunological response of the host.

SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY; HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane; Receptor; Repeat; Signal; TonB box;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            influenzae type b.";
Infect. Immun. 67:2729-2739(1999).
-!- FUNCTION: Acts as a receptor for hemoglobin or the
hemoglobin/haptoglobin complex of the human host and is required
for heme uptake.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=HIG89 / Serotype B; MEDLINE-99270928; Pubmed=10338475; MEDLINE-99270928; Pubmed=10338475; Morton D.J., Whitby P.W., Stull T.L.; Morton D.J. whitbje mutations in the hemoglobin-and hemoglobin-haptoglobin-binding proteins, HgpA, HgpB, and HgpC, of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
Hemoglobin and hemoglobin-haptoglobin
Homoglobin C.
Dinding protein C.
7 X 4 AA tandem repeats of Q-P-T-N.
                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last amoctation update)
Hemoglobin and hemoglobin-haptoglobin binding protein C precursor
                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IRR006970; PT.
InterPro; IRR006970; PT.
InterPro; IRR010949; TONB Box N.
InterPro; IRR010941; TONB Demiactrns.
InterPro; IRR010917; TONB Teceptor.
Pfam; PF04886; PT; II.
Pfam; PF040893; TONB dep Rec; I.
TIGRFAM8; TIGR01785; TONB-hemin; I.
TIGRFAM8; TIGR01786; TONB-hemin; I.
PROSITE; PS010196; TONB-DEPENDENT REC 1; PALSE_NEG.
                                                                                                                                                                                  PRT; 1066 AA.
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                                                             DYKIYPNKOAD 267
                                                                                                                                                                                  STANDARD;
                       DYKFYDNKRID 13
                                                                                                                                                                                                                                                                                                                    Name=hgpC;
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multigene family;
Transport.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=727;
                                                                                                                                                                                                                        16-OCT-2001
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                                                                257
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REPEAT
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Theor. Immun. 68:4092-4101 (2000)

Infect. Immun. 68:4092-4101 (20
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Interpro; IPR010916; TONB Box N.
Interpro; IPR010916; TONB Box N.
Interpro; IPR010919; TONB_Teceptor.
Interpro; IPR010917; TONB_Teceptor.
Interpro; IPR010917; TONB_Teceptor.
Interpro; IPR010917; TONB_Teceptor.
INTERPAMS; TIGR01785; TONB-hemin; 1.
TIGRPAMS; TIGR01786; TONB-hemin; 1.
TIGRPAMS; TIGR01786; TONB-hemin; 1.
TIGRPAMS; TIGR01786; TONB-DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Multigene family; Outer_membrane; Receptor; Repeat; Signal; TONB_DOX;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
6-UTL-2004 (Rel. 44, Last annotation update)
Hemoglobin and hemoglobin-haptoglobin binding protein B precursor (Hemoglobin binding protein B).
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                     Length 1066;
                                                                                                                                                                                                                                                                            Score 41; DB 1; Length 106
Pred. No. 3.3e+02;
1; Mismatches 3; Indels
                                                                                                                                               TonB C-terminal box.
MW; EFB88D5CE4247583 CRC64;
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7.
TonB box.
TonB C-te<sup>°</sup>
EFBP
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16-OCT-2001 (Rel. 40, Last sem
                  46 49
50 53
63 70
1049 1066
1066 AA; 122593 M
                                                                                                                                                                                                                                                                                 56.98;
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Matches 7; Conservative
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1066
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Q9KIV1;
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HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBFAMILY.
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61
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InterPro; IPR006970; PT
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Q89T91
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                                                                                                                                                                                                                                      Gaps
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Hemoglobin and hemoglobin-haptoglobin
Honding protein B.
6 X 4 AA tandem repeats of Q-P-T-N.
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Probable hemoglobin and hemoglobin-haptoglobin binding protein 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                         Score 41; DB 1; Length 1067;
Pred. No. 3.3e+02;
1; Mismatches 3; Indels
                                                                                                                                                    TonB box.
TonB C-terminal box.
MW; 29D295DC4747632E CRC64;
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                                                                                                                                                                                                                         63.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=HI0712;
                                                                                                                                                                                                                       Local Similarity 63.6
                                                                                                                                                                                                                                                                                           253 DYKIYPNKQAD 263
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                 3 DYKFYDNKRID 13
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1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                  1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                             HGP3 HAEIN
P44836;
                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor.
  Transport
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                          Query Match
                                                     DOMAIN
                                                                   REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04886; PT; 2.
Pfam; PF00593; TonB_dep_Rec; 1.
TIGRRAMs; TIGR01786; TonB-hemin; 1.
TIGRRAMs; TIGR01786; TonB-hemlactrns; 1.
PROSITE; PS00430; TONB_DEPENDENT REC 1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Complete protecome; Multigene family; Outer membrane; Receptor; Repeat;
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Probable hemoglobin and hemoglobin-
haptoglobin binding protein 3.
12 X 4 AA tandem repeats of O-P-T-N.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 3.4e+02;
; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-terminal box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TonB box.
                                                                                                                                                                                                                                                                                                                                                        interPro; IPR010949; TonB hemlactrns.
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                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000531; TonB_receptor.
InterPro; IPR010917; TonB_recept_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=22484998; PubMed=12597275;
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                                                                                                                                                                                                                                                                                                                             TONB BOX N.
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SIGNAL 1 24
CHAIN 25 1084
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                                                                                                                                                                                                                      EMBL; U32754; AAC22369.1; -.
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"Structural Analysis of Four Large Plasmids Harboring in a Unicellular Cyanobacterium, Synechocystis sp. PCC 6803.";
DNA Res. 10:221-228(2003).
EMBL; AP004310; BAD01784.1; -.
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Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                        Length 318;
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                                                                                                                                                                                                                                                     Query Match 55.6%; Score 40; DB 2; Length 318 Best Local Similarity 61.5%; Pred. No. 1.4e+02; Matches 8; Conservative 0; Mismatches 5; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ompA family.
EMBL, AK643794; AAT57676.1; --
INTERPOS INTERPOSE BAC OMPA.
InterPro; IPR006564; BAC OMPA.
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Pfam; PF01389; OmpA membrane; 1.
PRINTS; PR01021; OMPADOWAIN.
PRINTS; PR01022; OUTRMMBRANEA.
ProDom; PD00930; OmpA/MocB; 1.
PROSITE; PS01068; OMPA; 1.
SEQUENCE 349 AA; 37639 MW; 68E96F7EEAB47DC1 CRC64;
                                                                                                                                                                                  SEQUENCE 318 AA; 37404 MW; 453898D63373E55E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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77.8%; Pred. No. 1.5e+02;
tive 1; Mismatches 1;
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SEQUENCE FROM N.A.
STRAIN=T94289;
Akridge H., Confer A.W., Dabo S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR006690; OMPA_LIKE.
InterPro; IPR000498; OmpA_tmem.
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Pasteurellaceae, Pasteurella
NCBI_TaxID=747;
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                                                                                                                                                                                                                                                                                                                                                                                                     1 RSDYKFYDNKRID 13
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=95010872;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Segubs ;
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Q6GUB4
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           SXXXXX
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Matsumoto M., Shimpo S., Yamada M., Tabata S.;
"Structural analysis of four large plasmids harboring in a unicellular cyanobacterium, Synechocystis sp. PCC 6803.";
DNA Res. 10:221-228(2003).
EMBL, AP004310; BAD01784.1; -.
InterPro; IPR004860; LAGLIDADG_2.
Pfam; PF03161; LAGLIDADG_2; 1.
Complete proteome; Plasmid.
SEQUENCE 318 AA; 37404 MW; 453898D63373E55E CRC64;
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       Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005942; BAC47420.1; -.
Complete proteome.
SEQUENCE 172 AA; 19860 MW; 43126180BFC3FFA9 CRC64:
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Kaneko T., Nakamura Y., Sasamoto S., Watanabe A., Kohara M.,
Matsumoto M., Shimpo S., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                Ouery Match 55.6%; Score 40; DB 2; Length 172; Best Local Similarity 38.5%; Pred. No. 71; Matches 5; Conservative 6; Mismatches 2; Indels
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Plasmid pSYSM.
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
5115014 protein.
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OrderedLocusNames=sll5014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSDYKFYDNKRID 13
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67 KAAYRFFSNERVD 79
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BAD01784;
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062EWG
062EWG
AC 062EWG
DT 05-JU
DT 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

-: SIMILARITY: Belongs to the ompA family.

R EMBL, AY643798; AAT57680.1; -.

R InterPro; IPR006664; Bac CmpA.

R InterPro; IPR006665; OmpA.MotB.

R InterPro; IPR006669; OmpA.MotB.

R InterPro; IPR006699; OmpA.LIKE.

R InterPro; IPR00699; OmpA.LIKE.

R Pfam; PPC00891; OmpA.LIKE.

R Pfam; PPC010891; OmpA.LIKE.

R Pfam; PPC01021; OMPA.LIKE.

R Pfam; PPC01022; OUTRAMBRANEA.

R PFODOM; PD000930; OmpA.MotB; 1.

R PROSITE; PS01082; OMPA.MA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.6%; Score 40; DB 2; Length 353; Best Local Similarity 77.8%; Pred. No. 1.5e+02; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 55.6%; Score 40; DB 2; Length 353; Local Similarity 77.8%; Pred. No. 1.5e+02; les 7; Conservative 1; Mismatches 1; Indels
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 353 AA.
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QGGUBS
ID QGGUBS
AC GGGUBS
DT OS-JU
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Search completed: November 24, 2004, 09:28:55 Job time : 61.7717 secs

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; Search time 10.7391 Seconds (without alignments) 116.473 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                        November 24, 2004, 09:11:44
                                                                                    - protein search, using sw model
                       Copyright
                                                                                  OM protein
                                                                                                                          Run on:
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1 RSDYKFYDNKRID 13 US-09-719-379A-3 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 08 08 Minimum | Maximum | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	TonB-dependent rec	hemoglobin-binding	hemoglobin-binding	probable aspartate	hypothetical prote	probable transport	probable transport	probable transport	protein ZK809.1 [i	DNA-directed RNA p	hypothetical SPBC3	ORF MSV115 probabl	hemolysin B - Serr	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	cationic outer mem	probable shikimate	S-adenosylmethioni	hypothetical prote	cytochrome-c oxida	fumarate reductase	hypothetical prote	probable transport	aspartate-tRNA lig
01 0	2 H90200	2 G87372	2 B64083	2 B64088	2 T29857	2 T28007	1 F64782		2 G85550	2 F88843	2 T30681		2 T28276	2 B28182			2 D69957							2 \$73866	æ	1 S10164		2 T50054	2 AD3402
* Query Match Length DB	286	903	953	1084	408	428	437	463	463	466	1289	1646	505	557	264	266	638	740	921	144	159	170	207	220	246	256	325	507	595
Query Match	58.3	58.3	56.9	56.9		55.6	55.6			55.6					54.2		•	54.2		52.8		52.8		52.8	•	•	•	52.8	52.8
Score	42	42	41	41	40	40	40	40	40	40	40	40	σ	39.5		39			39	38	38	38	38	38	38	38	38	38	38
tesult No.	-	7	٣	4	ഗ	9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

lysine decarboxyla	lysine decarboxyla	lysine decarboxyla	androgen-regulated	pyruvate phosphate	pyruvate phosphate	lipoprotein [impor	beta-agarase - Vib	alpha-mannosidase	hypothetical prote	probable inorganic	hypothetical prote	hypothetical prote	inorganic diphosph	hypothetical prote	nodulin-31 precurs
B41842	G86108	A98268	S28259	AC1308	AC1680	G90563	S46651	S53048	T24222	H84561	B70116	E71646	S13379	G81264	842655
N	N	~	~	~	N	7	~	н	~	N	~	~	~	~	7
715	715	715	789	879	879	904	955	1083	1196	218	255	258	263	286	287
ω,	æ	8	80	80	80	8	80	80	80	4	4.	4.	4.	4	4.
52	22	52.8	52.8	22	52.8	52.8	52	22	52.8	5	5	5	51.4	51	21
38	38	38	38	38	38	38	38	38	38	37	37	37	37	37	37
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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CiSpecies: Sulfolobus solfataricus
CiSpecies: Sulfolobus solfataricus
CiDate: 24 May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
CiAccession: H90200
R;She, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, Q.; Singh, R.K.; Confalonieri, P.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Reference number: Appl39
A;Accession: H90200
hypothetical protein SSO0545 [imported] - Sulfolobus solfataricus
```

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-286 <KUR>

A;Cross-references: UNIPROT:Q9UWV0; GB:AE006641; NID:g13813707; PIDN:AAK40863.1; GSPDB:G: C;Genetics:

A; Gene: SS00545

ö Gaps ö 58.3%; Score 42; DB 2; Length 286; 53.8%; Pred. No. 14; 1; Live 3; Mismatches 3; Indels Query Match

1 RSDYKFYDNKRID 13 Conservative Best Local Similarity Matches 7; Conserv

:| | ||| :|| KSYYNFYDSSKID 65 δ g

TonB-dependent receptor, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87372
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-903 <STO>

A;Cross-references: UNIPROT:Q9A915; GB:AE005673; NID:g13422281; PIDN:AAK22979.1; GSPDB:G. C;Genetics: A; Gene: CC0995

ö Gaps ö Query Match 58.3%; Score 42; DB 2; Length 903; Best Local Similarity 66.7%; Pred. No. 42; Matches 8; Conservative 1; Mismatches 3; Indels a

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A;Residues: 11408 <WOH>
A;Cross-references: UNIPROT:Q22067; EMBL:U58726; PIDN:AAB00578.1; GSPDB:GN00028; CESP:TO
A;Experimental source: strain Bristol N2; clone T01C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Escherichia coli
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C; Accession: F64782
C; Accession: F64782
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
Science J.J.; Mau, B.; Shao, Y.
Science J.J.; Mau, B.; Shao, Y.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q23602; EMBL:Z68303; PIDN:CAA92641.2; GSPDB:GN00022; CESP:ZK A;Experimental source: clone ZK809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000157; GB:U00096; NID:g1786716; PIDN:AAC73613.1; PID:g1786721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZK809.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: aspartate aminotransferase
C;Keywords: aminotransferase; phosphoprotein; pyridoxal phosphate
F;251/Binding site: pyridoxal phosphate (Lys) (covalent) #status [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable transport protein b0511 - Escherichia coli (strain K-12)
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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            R;Wohldmann, P.; Hawkins, J. submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid TOICS.
A;Reference number: Z20699
                                                                                                                                                                A,Accession: T29857
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 2
Pred. No. 42; 2; Mismatches
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Pred. No. 44;
2; Mismatches
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A;Map position: 4
A;Introns: 2/2; 192/3; 358/3; 427/1
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 63.6%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 133/2; 257/1; 360/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SDYKF--YDNKRI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Gene: CESP: T01C8.5
C;Accession: T29857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hemoglobin-binding protein homolog H10712 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus
C;Accession: B64088
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A;Goncayne, J.D.; Schirley, R.; Liu, L.I.; Glodek, A.; Keiley, J.M.; Weidman, J.D.; Science 269, 496-512, 1995
A;Authors: Gambm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Retue: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: L-1084 *ITRR>
A;Residues: L-1084 *ITRR>
A;Cross-references: UNIPROT:P44836; GB:U32754; GB:L42023; NID:g1573711; FIDN:AAC22369.1;
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homology rINN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Start codon: GTG
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
F;1-130/Domain: tonB-dependent receptor amino-terminal homology <TNN>
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C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                 hemoglobin-binding protein homolog H10635 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 74;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 2; Length 953;
Pred. No. 65;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.9%;
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Local Similarity 63.6%;
nes 7; Conservative 1
                                                                                                        267 RADYKFDDNNSI 278
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Best Local Similarity 63.6
Matches 7; Conservative
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                                    1 RSDYKFYDNKRI
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Best Local S
Matches 7
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Afeference number: A;RoO0; MUID:199069613; PMID:9851916 A;Mote: see websites genome wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_eleA;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:Q23602; GB:Chr_IV; PIDN:CAA92641.1; PID:g3881799; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A/Reference number: Z20876; MUID:96325459; PMID:8670425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-directed RNA polymerase (EC 2.7.7.6) 146K chain - Molluscum contagiosum virus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T30881
R;Sentevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B. Science 273, 813-816, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          procein 2K809.1 [imported] - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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C;Superfamily: vaccinia virus DNA-directed RNA polymerase 147K chain
C;Keywords: nucleotidyltransferase; transcription
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A;Residues: 1-1289 <SEN>
A;Cross-references: UNIPROT:Q98246; EMBL:U60315; PIDN:AAC55207.1
         C;Superfamily: Escherichia coli probable transport protein b0511
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                                                                                                Length 463;
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                                                                                                                                                                                           Indels
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55.6%; Score 40; DB 2; 1
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 2;
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Pred. No. 48;
2; Mismatches
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                                                                                                7
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Science 282, 2012-2018, 1998
                                                                                           Score 40; DB 2
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.6%;
                                                                                                Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                414 DYKYYDN 420
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A,Molecule type: DNA
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D90700
probable transport protein EC80572 [imported] - Escherichia coli (atrain O157:H7, substr C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C; Accession: D90700
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: D90700
A; Residues: I-463 <HAV>
A; Residues: I-463 <HAV>
A; Residues: I-463 <HAV>
A; Residues: U-463 <HAV>
A; Residues: U-613 <HAV>
A; Residues: U-613 <HAV>
A; Residues: U-625 <U UNIPROT:Q8XCX4; GB:BA000007; PIDN:BAB33995.1; PID:gl3360030; GSPDB:G
C; Genetics:
C; Genetics:
C; Genetics:
C; Superfamily: Escherichia coli probable transport protein b0511
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G8550
probable transport protein Z0665 [similarity] - Escherichia coli (strain O157:H7, substr C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G8550
R;Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G8550
A;Accession: G8550
A;Accession: G8550
A;Residues: 1-463 <STO>
A;Residues: 1-463 <STO>
A;Cross-references: UNIPROT:Q8XCX4; GB:AE005174; NID:G12513405; PIDN:AAG54867.1; GSPDB:G;C;Genetics: A;Genetics: 
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         Experimental source: strain K-12, substrain MG1655
Superfamily: Escherichia coli probable transport protein b0511
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A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: Escherichia coli probable transport protein b C;Keywords: transmembrane protein
F;15-31/Domain: transmembrane #status predicted <TM1>F;8-98/Domain: transmembrane #status predicted <TM2>F;105-121/Domain: transmembrane #status predicted <TM3>F;105-121/Domain: transmembrane #status predicted <TM4>F;105-127/Domain: transmembrane #status predicted <TM5>F;105-1237/Domain: transmembrane #status predicted <TM6>F;201-237/Domain: transmembrane #status predicted <TM6>F;201-237/Domain: transmembrane #status predicted <TM7>F;304-320/Domain: transmembrane #status predicted <TM8>F;304-320/Domain: transmembrane #status predicted <TM10>F;304-321/Domain: transmembrane #status predicted <TM10>F;304-321/Domain: transmembrane #status predicted <TM10>F;305-321/Domain: transmembrane #status predicted <TM10>F;405-421/Domain: transmembrane #status predicted <TM11>F;405-421/Domain: transmembrane #status predicted <TM11>F;405-4
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1; Mismatches
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Best Local Similarity 85.77
داره 6، Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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414 DYKYYDN 420
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A;Cross-references: UNIPROT:P15321; GB:M22618; NID:g340726; PIDN:AAA50322.1; PID:g556419
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: G82939
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. aubmitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Accession: G82939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA-
A;Residues: 1-264 <GLA>
A;Cross-references: GB:AE002105; GB:AF222894; NID:g6899003; PIDN:AAF30466.1; GSPDB:GN001.
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein orf266 [imported] - Guillardia theta nucleomorph C; Species: nucleomorph Guillardia theta
C; Species: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C; Anotes a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C; Accession: D90131
C; Accession: D90131
Nature 410, 1091-1096, 2001
Nature 410, 1091-1096, 2001
A; Title: The highly reduced genome of an enslaved algal nucleus.
A; Reference number: A99082; MUID:11323671; PMID:11323671
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A;Molecule type: DNA
A;Residues: 1-266 < DOUJ>
A;Cross-references: UNIPROT:Q98S40; GB:AF083031; NID:g13794366; PIDN:AAK39743.1; GSPDB:G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical UU061 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                DB 2; Length 557;
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Pred. No. 41;
1; Mismatches
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                                                                                                                                                             Score 39.5; D
Pred. No. 69;
2; Mismatches
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Best Local Similarity 64.3%;
Matches 9; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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133 DYKFYEN 139
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                         A, Residues: 1-557 < POO>
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ORF MSV115 probable vaccinia G5R homolog - Melanoplus sanguinipes entomopoxvirus
C,Species: Melanoplus sanguinipes entomopoxvirus
C,Species: Melanoplus sanguinipes entomopoxvirus
C,Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C,Accession: T28276
R,Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A,Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A,Reference number: 220484; MUID:99102612; PMID:9847359
A,Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A,Reference number: 220484; MUID:99102612; PMID:9847359
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rocession: T28276
A,Status: preliminary
A,Molecule type: DNA
A,Redeatious: 1-505 <ARO>
A,Cross-references: UNIPROT:Q9YVX7; EMBL:AF063866; NID:g4049647; PIDN:AAC97659.1; PID:g4
C,Genetics:
A;Note: MSV115
C;Superfamily: vaccinia virus probable 49.8K protein
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T40198; T40630
R;Oliver. X.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, March 1999
A;Recence number: 221912
A;Recession: T40199
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recession: T40199
A;Residues: 1-1595 cOLI>
A;Residues: 1-1595 cOLI>
A;Residues: 1-1595 cOLI>
A;Residues: 1-1595 cOLI>
A;Residues: 1-1595 coll
A;Residues: 1-1505 coll
A;Residues: 1-1505 coll
A;Residues: 1505-1646 clrN>
A;Residues: 1596-1646 clrN>
A;Residues: 1596-1646 clrN>
A;Residues: 1596-1646 clrN>
A;Residues: 1596-1646 clrN>
A;Residues: 1506-1646 clrN>
A;Residues: 1506-
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1928182
hemolygin B - Serratia marcescens
C;Species: Serratia marcescens
C;Species: Serratia marcescens
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
R;Poole, K.; Schlebel, E.; Braun, V.
J. Bacteriol. 170, 3177-3188, 1988
A;Title: Molecular characterization of the hemolysin determinant of Serratia marcescens.
A;Reference number: A28182; MUID:88257037; PMID:3290200
A;Accession: B28182
A;Molecule type: DNA
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Pred. No. 1.6e+02;
3; Mismatches 2; Indels
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60.0%; Pred. No. 63;
Live 1; Mismatches
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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A; Map position: 2
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A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72301
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72301
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                CjAccession: AE0332
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Akeference number: AB0001; MUID:21470413; PMID:11586360
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 125 - Melanoplus sanguinipes entomopoxvirus
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T28286
R;Afonso, C.L.; Tulman, B.R.; Lu, Z.; Oma, B.; Kutish, G.F.; Rock, J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus. A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cationic outer membrane protein - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2; 1
Pred. No. 1.4e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-144 <AFO>
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Pred. No. 33;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.2%;
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50.0%;
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDFKIYQNKNV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SDYKFYDNKRI 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : || |:||:|
KKDYYIYNNKKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Status: preliminary
A, Molecule type: DNA
A, Residues: 1-159 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-921 < KUR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: YP02725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: MSV125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 21
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                                                Conserved hypothetical protein yggs - Bacillus subtilis
C;Species: Species: Speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q20760; EMBL:249967; PIDN:CAA90257.1; GSPDB:GN00020; CESP:F5
A;Experimental source: clone F54C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P54496; GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14415.
A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE0332
conserved hypothetical protein YPO2725 [imported] - Yersinia pestis (strain CO92)
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A,Introns: 28/3; 46/1; 140/2; 169/2; 257/2; 295/3; 409/3; 481/1; 651/3; 705/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F54C9.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22G38
R;Sims, M.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19591
A;Reference number: Z19591
A;Recession: T22G38
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: Bacillus subtilis probable anion-binding protein yflE
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Pred. No. 1.1e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 638
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Pred. No. 96;
2; Mismatches
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-740 <WIL>
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A; Residues: 1-638 < KUN>
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Gaps

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C; Species: Mycoplasma pneumoniae
A; Variety: ATCC 29342
C; Date: 2.7-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: 873866
R; Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A; Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A; Reference number: 873327; MUD:97105885; PMID:8948633
A; Accession: 873866
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P75482; EMBL:AE000053; GB:U00089; NID:g1674236; PIDN:AAB9618.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytochrome-c oxidase (EC 1.9.3.1) fixO chain - Azorhizobium caulinodans
N;Alternate names: cb-type cytochrome-c oxidase 28K chain; cytochrome b410; fixO protein!
S;Species: Azorhizobium caulinodans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: B55582; S42230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Modecule type: DNA
A; Residues: 1-246 < CMAN1>
A; Cross-references: UNIPROT: Q43943; GB: X74410; NID: g455110; PIDN: CAA52430.1; PID: g456312
B; Mandon, K.; Kaminski, P.A.; Mougel, C.; Desnoues, N.; Dreyfus, B.; Elmerich, C.
FEMS Microbiol. Lett. 114, 185-190, 1993
A; Title: Role of the fixcHI region of Azorhizobium caulinodans in free-living and symbio.
A; Reference number: S42229; MUID: 94109675; PMID: 8282187
A; Accession: S42230
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross-references: EMBL:X74410; NID:g456310; PIDN:CAA52430.1; PID:g456312
A;Orcoss-references: EMBL.X74410; NID:g456310; PIDN:CAA52430.1; PID:g456312
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993
C;Superfamily: Rhizobium cytochrome-c oxidase fixO chain
C;Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory
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J. Bacteriol. 176, 2560-2568, 1994
A;Title: Functional analysis of the fixNOOP region of Azorhizobium caulinodans.
A;Reference number: A55582; MUID:94222833; PMID:8169204
A;Accession: B5582
                                                                                                                                                                                                                                                                                                                         hypothetical protein H10_orf220L - Mycoplasma pneumoniae (strain ATCC 29342)
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                                                                  Length 207;
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Pred. No. 50;
1; Mismatches
                                                                Score 38; DB 2
Pred. No. 48;
2; Mismatches
A, Gene: CAC3419
C, Superfamily: spore germination protein C2
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75.0%;
                                                                  52.8%;
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Similarity 54.5%;
6; Conservative
                                                                                                                                                                                                           167 KGDYKLYSKKEIE 179
                                                                                                                                                             1 RSDYKFYDNKRID 13
                                                                                                                Conservative
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                                                                Query Match
Best Local Similarity
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Best Local Similarity
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A;Start codon: TTG
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Best Local S:
Matches 6,
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                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                     RESULT 23
B97320
S-adenosylmethionine-dependent methyltransferase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 12-Jul-2004
C;Accession: B97320
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Barty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4832-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325, PMID:21359325
A;Accession: B97320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-207 <KUR>
A;Cressore references: UNIPROT:Q97DQ3; GB:AE001437; PIDN:AAK81349.1; PID:g15026507; GSPDB:C
C;Genetics:
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Pred. No. 39;
                                               Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                          Indels
                                             Score 38; DB 2;
Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                          Mismatches
                                             52.8%;
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66.7%;
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                                                                                        Conservative
                                                                                                                                                                  : || || ||
54 KRDYSFYQNK 63
                                                                                                                                     1 RSDYKFYDNK 10
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28 RLDYRFYDS 36
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Best Local Similarity
Matches 6; Conserv
                                        Query Match
Best Local Similarity
Matches 6; Conserv
A;Gene: TM1053
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aspartate-tRNA ligase (BC 6.1.1.12) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: D. Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AD3402
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD325; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Crose-references: UNIPROT:Q8YGF7; GB:AE008917; PIDN:AAL52383.1; PID:g17983182; GSPDB:G
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross references: UNIPROT: Q9US37; EMBL: AL133521; PIDN: CAB63540.1; GSPDB: GN00066; SPDB: A; Experimental source: strain 972h(-); cosmid c1039
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C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B41842; S094017; $56360; A41968; B65223
K;Meng, S.Y.; Bennett, G.N.
J. Bacteriol. 174, 2659-2669, 1992
                                                                                                                                                                                                  probable transporter [imported] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: O9-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                              C;Accession: T50054
R;Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitred to the EMBL Data Library, December 1999
A;Reference number: Z5031
A;Accession: T50054
A;Accession: T50054
A;McLeus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-507 < HUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 2; Dred. No. 1.1e+02; 2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: I
C;Superfamily: lysine-tRNA ligase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.8%;
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SVYMFFDNRRRD 477
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                      104 DYKFYDD 110
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Best Local Similarity
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A;Map position: 1
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A;Residues: 1-595 <KUR>
3 DYKFYDN
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C;Species: Wolinella succinogenes
C;Species: Wolinella succinogenes
C;Species: Wolinella succinogenes
C;Species: 12.Nov-1993 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: S10164; A44954
R;Koertner, C.; Lauterbach, F.; Tripier, D.; Unden, G.; Kroeger, A.
Mol. Microbiol. 4, 885-866, 1990
A;Title: Wolinella succinogenes fumarate reductase contains a dihaem cytochrome b.
A;Reference number: S10164; MUID:90355847; PMID:2388563
A;Accession: S10164
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-256 <KOE>
A;Tensernces: UNIPROT:P17413; EMBL:X51509; NID:948511; PIDN:CAA35874.1; PID:948512
R;Lauterbach, F.; Koertner, C.; Albracht, S.P.J.; Unden, G.; Kroeger, A.
Arch. Microbiol. 154, 386-393, 1990
A;Title: The fumarate reductase operon of Wolinella succinogenes. Sequence and expressic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypotherical protein BH4011 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Ol-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C84151
R;Takami, H:; Nakasone, K:; Takaki, Y:; Maeno, G:; Sasaki, R:; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Complex: part of an enzyme complex containing a heterotrimer (flavoprotein, iron-sulfe
C;Punction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: catalyzes the oxidation of succinate to fumarate and transfers its reducing the complex together with the iron sulfur subunit (5)Superfamily: fumarate reductase, cytochrome b subunit (5)Superfamily: fumarate transmembrane protein; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Regidues: 1-325 <STO>
A; Residues: 1-325 <STO>
A; Cross-references: UNIPROT:Q9KSS7; GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB077
A; Groserimental source: strain C-125
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                               fumarate reductase (EC 1.3.99.1) cytochrome b component - Wolinella succinogenes N/Alternate names: fumarate reductase chain C
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85.7%; Pred. No. 74;
tive 1; Mismatches 0; Indels
   IndelB
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Mismatches
1;
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6; Conservative
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A;Molecule type: DNA
Residues: 205-256 cLAU>
A;Cross-references: GB:X51509
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244 DYKYFDYKR 252
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                                                      DYKFYDNK 10
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Matches
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3; Indels

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A;Status: preliminary
A;Molecule type: DNA
A;Reaidues: 1-715. cSTO-
A;Cesidues: 1-715. cSTO-
A;Cesidues: 1-715. cSTO-
A;Cesidues: 1-715. cSTO-
A;Cesidues: 1-715. cSTO-
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
              A,Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A,Reference number: A85480; MUID:21074935; PMID:11206551
A,Accession: G86108
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                                                                                                                                                                                                                                                                               A;Gene: cadA
C;Superfamily: ornithine/lysine/arginine decarboxylase
                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 2;
Pred. No. 1.6e+02;
2; Mismatches 3
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58.3%;
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Best Local Similarity be...
7; Conservative
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575 REDPEFYENMRI 586
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REDPEFYENMRI 586
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nes 7; Conserv
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A, Residues: 1-715 < HAY>
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Aritle: Nucleotide sequence of the Becherichia coli cad operon: a system for neutralizative control of the sequence of the Becherichia coli cad operon: a system for neutralizative communication of lact the sequence of 
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g86108
1ysine decarboxylase 1 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G86108
R;Perasi N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
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Pred. No. 1.6e+02;
2; Mismatches 3; Indels
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Matches 7; Conservative
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lysine decarboxylase I [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050 C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Bacherichia coli C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: A98268 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Feference number: A99629; MUID:21156231; PMID:11258796 A;Accession: A98268 A;Accession: A98268 A;Accession: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:P23892; GB:BA000007; PIDN:BAB38536.1; PID:g13364590; GSPDB:G
A,Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: 528259
R;Perry, A.C.F.; Jones, R.; Barker, P.J.; Hall, L.
Bochem. J. 286, 671-675, 1992
A;Title: A mammalian epididymal protein with remarkable sequence similarity to snake ver A;Reference number: S28258; MUID:93038491; PMID:1417724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q63180; EMBL:X66140; NID:g56069; PIDN:CAA46930.1; PID:g56070 C;Superfamily: mouse meltrin alpha; disintegrin homology C;L25/Domain: signal sequence #status predicted <8IG>F1.25/Domain: signal sequence #status predicted <8IG>F26-789/Product: androgen-regulated epididymal protein #status predicted <MAT>F336/Region: defective catalytic site F;336/Region: defective catalytic site F;400-482/Domain: disintegrin homology <DIS>
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C;Date: 17-Apr_1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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C;Superfamily: ornithine/lysine/arginine decarboxylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.8%; Score 38; DB 2; I 58.3%; Pred. No. 1.6e+02; iive 2; Mismatches 3;
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Lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Accession: G90563
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-904 «KUT»
A;Cross-references: UNIPROT:0980F1; GB:AL445566; PID:g14089829; PIDN:CAC13588.1; GSPDB:G
A;Experimental source: strain UAB CTIP
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A)Residues: 1-955 <800>
A)Cross-references: UNIPROT:P48840; EMBL:D21202; NID:g498302; PIDN:BAA04744.1; PID:g5312
A)Cross-references: UNIPROT:P48840; EMBL:D21202; NID:g498302; PIDN:BAA04744.1; PID:g5312
A)Experimental source: atrain J10107
B) Sugano, Y: Matsumoto, T: Noma, M.
B) Sochim. Biophys. Acta 1218, 105-108, 1994
A)71tle: Sequence analysis of the agaB gene encoding a new beta-agarase from Vibrio sp. A)Accession: 84226
A)Accession: 8422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deta-agarase - Vibrio sp. (strain JT0107)
CiSpecies: Vibrio sp.
A;Variety: strain JT0107
A;Variety: strain JT0107
C;Accession: S4651; S45296
C;Accession: S4651; S45296
R;Sugano, Y.; Mateunco, T.; Noma, M.
B;Ubmitted to the EMBL Data Library, October 1993
A;Reference number: S46551
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NiAlternate names: protein G1861; protein YGL156w
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Species: OS-May-2000 #sequence_revision OS-May-2000 #text_change 09-Jul-2004
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3; Mismatches 2;
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Pred. No. 2e+02;
4; Mismatches
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ilarity 54.5%;
Conservative 3
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50.0%;
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235 RKEYKFDENRKI 246
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C,Superfamily: Vibrio agarase
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Best Local Similarity
6; Conserve
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Best Local Similarity
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A;Genetic code: SGC3
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S53048
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                                                                                                                                                                                                                                                                                                                                                                                                   AC1308
pyruvate phosphate dikinase homolog lmo1867 [imported] - Listeria monocytogenes (strain C; Species: Listeria monocytogenes
C; Species: Listeria monocytogenes
C; Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: AC1308
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Attchers number: AB1077; MUD:21537279; PMID:11679669
A; Accession: AC1308
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Residues: 1-879 cGLA>
A; Rosidues: 1-879 cGLA>
A; Rosidues: 1-879 cGLA>
A; Experimental source: strain EGD-e
C; Genetics: Agenerics: Uniper DNA
A; Genetics: Limo1867
C; Superfamily: pyruvate, phosphate dikinase
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A;Experimental source: strain Clip11262
A;Gene:1ca: A;Gene:1an981
C;Superfamily: pyruvate, phosphate dikinase
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50.0%; Pred. No. 1.9e+02;
iive 4; Mismatches 2; Indels
                                                       3; Indels
         Pred. No. 1.7e+02; 3; Mismatches 3
50.0%;
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399 NDYPFCGNKKVD 410
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| 561 RTEHMFFDEKRI 572
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561 RTEHMFFDEKRI 572
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    Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A; Accession: H84561
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C;Accession: 860420; A33511; 864172; 853048
Yeast 11, 1413-1419; 1955
Yeast 11, 1413-1419; 1955
Yeast 11, 1413-1419; 1955
A;Title: DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosc A;Title: DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosc A;Title: DNA sequence analysis of a 35 kb segment from solding sides and solding sides and sequence analysis of a 35 kb segment from solding sides a 360417; MUD:95158061; PMID:9585324
A;Accession: 860407; MUD:95158061; PMID:9528690; PIDN:CAA86536.1; PID:97286
A;Accession: Asia c/AMA.
A;Kesidues: 1-1083 c/AMA.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
B;Yoshihisa: T: Annaku. Y.
A;Note: the nucleotide sequence of ANSI, the structure gene of vacuolar alpha-mannosidase capacter of a 3514 sides and sides a 3616 sides a 3617 sides a 3618 sides a 36
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T2422
R;Kershaw, J.
submitted to the EMBL Data Library, November 1996
A;Recence number: Z19858
A;Accession: T2422
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T2422
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Recession: T2422
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1196 (WIL)
A;Rosidues: 1-1196 (WIL)
A;Experimental source: clone R13H4
C;Genetics:
A;Gene: CESP:R1H4.1
A;Map position: 5
A;Introns: 42/3; 70/1; 109/2; 173/1; 235/3; 281/2; 572/2; 632/3; 725/1; 857/1; 1068/2; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 52.8%; Score 38; DB 2; Length 1196; Local Similarity 66.7%; Pred. No. 2.6e+02; hes 6; Conservative 2; Mismatches 1; Indels
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probable inorganic pyrophosphatase [imported] - Arabidopsis thaliana
C;Specides: Arabidopsis thaliana (mouse-ear cress)
C;Specides: Arabidopsis thaliana (mouse-ear cress)
C;Date (10.2 Pcb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H94561
R;Lin, X:, Rounla, R; Rounla, P., Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Recession: H94561
A;Retaus: preliminary
A;Nolecule type: DNA
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Residues: 1-218 < STO>
A;Residues: 1-218 < STO
A;Re
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                          OM protein - protein search, using sw model
                      Copyright
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Run on:

November 24, 2004, 09:07:49; Search time 82.8152 Seconds (without alignments) 82.302 Million cell updates/sec

US-09-719-379A-1 Title: Perfect score:

105 1 RSDYKFYEAANGTRDHKKG 19 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2002273 segs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

2002273

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* 1: qeneseqp1980s:* geneseqp1980s:* geneseqp1990s:* Database

geneseqp20008:* geneseqp20018:* geneseqp20028:* geneseqp2003a8:* geneseqp2003b8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20048:*

## SUMMARIES

	tion .	9 Non-typea		-	_		-			-		_		2 Chimeric	1 H. influe	4 Non-typab		7 Non-typea						7 Non-typea		
•	Description	Aay79959	Aay79987	Aay79960	Aay79961	Aay 79982	Aay79991	Aay 79955	Aab47439	Aab20881	Aab47443	Aaw67581	Aay79986	Ada25172	Adc89661	Aar66294	Aay79993	Aay79957	Aay79963	Aay79958	Aay79956	Aaw67572	Ada25163	Aay79967	Aay79968	Aay79973
SUMMAKIES	ID	AAY79959	AAY79987	AAY79960	AAY79961	AAY79982	AAY79991	AAY79955	AAB47439	AAB20881	AAB47443	AAW67581	AAY79986	ADA25172	ADC89661	AAR66294	AAY79993	AAY79957	AAY79963	AAY79958	AAY79956	AAW67572	ADA25163	AAY79967	AAY79968	AAY79973
	DB	, m	ო	٣	m	٣	٣	٣	4	m	4	~	m	9	7	~	m	m	m	m	m	~	9	m	m	m
	Query Match Length	13	19	19	19	19	19	19	19	20	28	40	40	40	40	359	464	19	19	19	19	18	18	19	19	19
de	Query	100.0	100.0	96.2	95.2	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	94.3	91.4	90.5	89.5	89.5	98.6	88.6	86.7	86.7	85.7
	Score	105	105	101	100	66	66	66	66	66	66	66	66	66	66	66	66	96	95	94	94	93	93	91	91	90
	Result No.	-	7	'n	4	S	ø	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aay79970 Non-typea	Aay79966 Non-typea	Aay79962 Non-typea	_	Aay79971 Non-typea	_		_	Aar85450 Nontypabl	Adc89652 H. influe	Aay79972 Non-typea	Aag45896 Arabidops	Aag34578 Arabidops	Aag20945 Arabidops	Aag45883 Arabidops	Aag24458 Arabidops	Aag20944 Arabidops	Aag24457 Arabidops	Aag45882 Arabidops	Aag45881 Arabidops
AAY79970	AAY79966	AAY79962	AAY79965	AAY79971	AAY79992	AAY79964	AAY79969	AAR85450	ADC89652	AAY79972	AAG45896	AAG34578	AAG20945	AAG45883	AAG24458	AAG20944	AAG24457	AAG45882	AAG45881
19 3	19 3	19 3	19 3	19 3	19 3	19 3	19 3		18 7	19 3	311 3	343 3	361 3	٠.	361 3	•	٠.	378 3	414 3
84.8	84.8	83.8	83.8	81.9	81.0	81.0	80.0	80.0	79.0	76.2	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7	45.7
83	83	88	88	98	82	82	84	84	83	80		48	48	48	48	48	48	48	48
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Vaccine, non-typeable Haemophilus influenzae, ntH1; infection; chimeric protein, Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower zespiratory tract infection. Non-typeable H. influenzae group 1 LB1(f) peptide N10567RM. AAY79959 standard; peptide; 19 AA 15-MAY-2000 (first entry) AAY79959; 

Haemophilus influenzae.

WO9964067-A2.

16-DEC-1999

99WO-US011980. 28-MAY-1999;

98GB-00012613 11-JUN-1998; (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.

Lobet Bakaletz LO, Cohen J, Dequesne G,

WPI; 2000-116457/10.

antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza. Novel

Example 1; Page 29; 68pp; English.

The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinustis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae and probes from the present invention can be used for diagnosis of H. influenzae infection. AAX79955 to AAX79953, and AAX291201 to AAX21252, represent sequences used in the exemplification of the present invention

Matches

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RESULT 2 AAY79987

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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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                                                                                                                             Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Haemophilus influenzae; PS-INke fimbrin protein; lipoprotein D; LBJ(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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chimeric protein; Haemophilus influenzae; PS-like fimbrin protein;
lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis;
conjunctivitis; lower respiratory tract infection.
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                                                                                         Non-typeable H. influenzae group 1 LB1(f) peptide N86027NP.
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                                                     (first entry)
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               AAY79960;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
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                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Hemophilus influenzae, PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                 100.0%; Score 105; DB 3; Length 19; 100.0%; Pred. No. 3.6e-11;
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Best Local Similarity
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nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1998;
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Sequence 19
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                                   Query Match
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Matches

8 셤 RESULT 3 AAY79960 ID AAY7

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AAY79991 standard; peptide; 19 AA
                                                 Example 1; Page 30; 68pp; English
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                                                                                                                                                                                                                                                                                                    1 RSDYKFYEAANGTRDHKKG 19
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                                                                                                                                                                                                                                                            18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
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                                                                                                                                                                                   the present invention
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                                                                                                                                                                                                                                               Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                             Sequence 19 AA;
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                                                                                                                                                                                 Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                                                                      The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79993, and AAZ91201 to AAZ91222, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           ch 95.2%; Score 100; DB 3; Length 19; I Similarity 94.7%; Pred. No. 2.7e-10; 18; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-typeable H. influenzae group 1 LB1(f) peptide N1128.
                                                                                                                                     Lobet Y;
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                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
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                                                                                                                                   Dequesne G,
                                                                                                                                                                                                                       Example 1; Page 29; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY79982 standard; peptide; 19 AA
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                                               99WO-US011980
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                                                                                                                                  Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae
                                                                                                                                                                                                Haemophilus influenza.
                                                                                                                                                           WPI; 2000-116457/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                                                                                                                                  Bakaletz LO,
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                                                                       11-JUN-1998;
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                        16-DEC-1999.
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Novel antigenic Ps-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
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                                                                                                                                                                                                                                                The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Hamophilus influenzae strains. The peptides are used for disgnosis, prevention, and treatment of Hamophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae, Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. ANY19955 to ANY19931, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY19955 to AAY19993, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.3%; Score 99; DB 3; Length 19; 94.7%; Pred. No. 4.1e-10; ive 0; Mismatches 1; Indels
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us-09-719-379a-1.rag

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AAB47439 standard; peptide; 19 AA.
                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                          media and conjunctivitis.
                                                                                                                                                                                                                                                                                                           Denoel P,
                                                                                                                                                                      Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                                                                                                                                                                                             WO200161013-A1.
                                                                                                                                                                                                                                                                                                           Berthet FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2001
                                                                  31-OCT-2001
                                                                                                                                                                                                                   23-AUG-2001
                                             AAB47439;
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Matches
 RESULT 8
           AAB47439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAV79955 to AAV79993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
AAZ91201 to AAZ91252, represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                         Vaccine, non-typeable Haemophilus influenzae, ntHi; infection, chimeric protein, Haemophilus influenzae, PS-like fimbrin protein, lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                      Score 99; DB 3; Length 19; Pred. No. 4.1e-10; O: Mismatches 1; Indels
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                                                                                                                                                                                                                                                    Non-typeable H. influenzae group 1 LB1(f) peptide N1128.
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larity 94.7%; Pred. No. 4.1e-10;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lobet Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
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                                                                                                                                                                                 AAY79955 standard; peptide; 19 AA
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                                                                                                                1 RSDYKFYEDANGTRDHKKG 19
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                                                       94.3%;
                                                                                                                                                                                                                              (first entry)
                                                                 1 Similarity 94.7
                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bakaletz LO, Cohen J,
           the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-116457/10.
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nes 18; Conserv
                                 Sequence 19 AA;
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Best Local S
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The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein PS (MOMP PS) of non-typeable H. influenzae (ntHi). Each of these peptides contain an LB1 () peptide which is a 19 amino acid peptide derived from the sequence of MOMP PS from strain ntHill28, representing amino acids Argl17 to G1V13. This peptide represents the third exposed loop of PS and is a potential B call epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant bacterial outer membrane protein where one or more surface exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
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                                                                          surface exposed loop, major outer membrane protein P5; MOMP P5;
non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope,
otitis media; sinusitis; conjunctivitis;
lower respiratory tract infection.
LB1(f) containing peptide from strain ntHi-1128 (Group 1 type).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poolman J, Thonnard J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an immunogen (1) comprising a peptide (1a) and a carrier (1b) derived from protein D of Haemophilus influenzae (1a) and a carrier. Also described are: (1) a vaccine comprising (1), and an excipient; (2) preparation of (1), comprising conjugating a peptide to protein D or its fragment; and (3) preparation of a vaccine of (1), comprising formulating (1) with an excipient. (1) has cytostatic, comprising formulating (1) with an excipient. (2) preventing and treating infectives and protozoacide activities. (1) and the vaccine are useful for the manufacture of a medicament for and the vaccine are useful for the manufacture of a medicament for chasease such as and treating infectious diseases or allergy in a patient. Unlike prior art immunogens, (1) induces high levels of antipeptide immuno responses while inducing a moderate humoral response against the carrier. The present sequence represents an LB1grl peptide which was coupled through an additional C-terminal cysteine via maleimide to protein D in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                      Immunogens and vaccine comprising the immunogen useful for preventing and treating infectious diseases e.g. malaria and chronic disease e.g. cancer, comprises peptide and carrier from protein D of influenzae.
prostate cancer, Haemophilus influenzae; vaccine; infectious disease; malaria; cytostatic; antiallergic; nootropic; neuroprotective; protozoacide; Alzheimer's disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
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                                                                                                                                                                                                                                                                                                                       Coste M, Lobet Y, Van-Mechelen MP, Verriest C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99; DB 3; I
Pred. No. 4.4e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                            Location/Qualifiers
                                                                                                   'note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 14; Page 34; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB47443 standard; peptide; 28 AA
                                                                                                                             /note= "amidated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSDYKFYEAANGTRDHKKG 19
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                                                                                                                                                                                                                                           99GB-00004408.
99GB-00004412.
99GB-00019260.
                                                                                                                                                                                                      22-FEB-2000; 2000WO-EP001457.
                                                                                                                                                                                                                                99GB-00004405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                              WPI; 2000-572040/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20 AA;
                                                                                                                                                     WO200050077-A1
                                                                                       Modified-site
                                                                                                              Modified-site
                                                                                                                                                                                                                                            25-FEB-1999;
25-FEB-1999;
                                                                                                                                                                                                                               25-FEB-1999;
                                                                                                                                                                                                                                                                     13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-2001
                                                                                                                                                                              31-AUG-2000
                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB47443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB47443
셤
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The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein PS; (MOMP PS) of non-typeable H. influenzae (ntHi). Each of these peptides contain an LBI(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP PS from strain ntHill28, representing amino acids Argll7 to Gly135. This peptide represents the third exposed loop of PS and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Haemophilus sinfluenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant bacterial outer membrane protein where one or more surface-
exposed loops are modified is useful as a vaccine to prevent or treat
Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-typable Haemophilus influenzae; fimbrin; T-cell epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic chimer fimbrin/T-cell epitope peptide LB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 99; DB 4; I
Pred. No. 6.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                 Poolman J, Thonnard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenic composition; immune response
                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW67581 standard; peptide; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00460502.
                                                                                                                                                                                                                                            13-FEB-2001; 2001WO-EP001556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.3%;
ilarity 94.7%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-00460502
                                                                                                                                                                                                                                                                                       15-FEB-2000; 2000GB-00003502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                media and conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                 Denoel P,
                                                                                                Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-522599/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28 AA;
                                                                                                                                                WO200161013-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5843464-A
                                                                                                                                                                                              23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                   Berthet FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW67581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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Gaps

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prevention, and treatment of Haemonphilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. finfluenzae antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAS91201 to AAX91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a synthetic chimeric fimbrin peptide. The peptide is useful for treating a non-typable Haemophilus influenzae (NTH) infection and otitis media. The synthetic peptides do not require tedious purification techniques. The present sequence represents the amino acid sequence of the chimeric fimbrin peptide LB1.
 Haemophilus influenzae strains. The peptides are used for diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic chimeric fimbrin peptide, useful for treating Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                              fimbrin; non-typable Haemophilus influenzae; NTHi infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.3%; Score 99; DB 6; Length 40; ilarity 94.7%; Pred. No. 9.9e-10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                      Length 40;
                                                                                                                                                                                                  1; Indels
                                                                                                                                                                     Score 99; DB 3; I
Pred. No. 9.9e-10;
                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                       ADA25172 standard; peptide; 40 AA
                                                                                                                                                                                                                                                            19
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                                                                                                                                                                                                                                1 RSDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Col 4; 16pp; English
                                                                                                                                                                     94.3%;
                                                                                                                                                                                                                                                   98US-00148711.
                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric fimbrin peptide LB1
                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003 (first entry)
                                                                                                                                                             Ouery Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bakaletz LO, Kaumaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    influenzae infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-615247/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                        Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Measles virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6436405-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                     ADA25172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric.
                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                          ADA25172
 888888888888
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                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                              The invention relates to the manufacture of a synthetic chimeric peptide comprising a non-typable Haemophilus influenzae fimbrin peptide fused via a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce an immune response against non-typable Haemophilus influenzae. This sequence represents an example of a chimeric fimbrin/T-cell epitope peptide and is designated LB1. The peptide comprises a 19 amino acid sequence corresponding to amino acids 117-135 of the fimbrin protein, the linker sequence and amino acid 288-302 of the measles virus fusion protein (a T-cell epitope)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                        Synthetic chimeric fimbrin peptide - useful for vaccination against non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Hampinilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                    Score 99; DB 2; Length 40;
Pred. No. 9.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Measles virus fusion protein T-cell promiscuous epitope,
                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY79986 standard; peptide; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 38; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSDYKFYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSDYKFYEAANGTRDHKKG 19
                                                                                                                          typable Haemophilus influenzae
                                                                                                                                                     Claim 4; Col 4; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                 94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98GB-00012613
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                                            PTP, Bakaletz LO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  18; Conservative
               (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-116457/10.
                                                                          WPI; 1999-044514/04
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Measles virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bakaletz LO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                              Kaumaya
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Fimbrin protein; vaccine; otitis media.
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                                                                                                               WO9426304-A1
                                                                                                                                                           12-MAY-1994;
                                                                                                                                                                                 18-MAY-1993;
                                                                                                                                     24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY79993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                              Peptide
                                              Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a synthetic chimaeric fimbrin peptide LB1 or LB2 comprises a first peptide unit derived from H. influenzae fimbrin, a second peptide unit containing a T cell eptcope and a third linker peptide which connects the first peptide to the second. The chimaeric peptide which connects the first peptide to the second. The chimaeric peptide is useful for inducing an immune response in animals against nontypable Haemophilus influenzae (NTHi) and for preventing or reducing adherence of NTHi to host cells thereby preventing or reducing the severity of otitis media. The present sequence is an H. influenzae fimbrin peptide/measles virus T cell epitope chimaeric peptide of the invention, LB1.
                                                                                                                                                                                                                                                                                                                                                                             Novel synthetic chimeric fimbrin peptide LB1 or LB2 comprising a first peptide unit, T cell epitope as second peptide unit and third linker peptide unit, useful for preventing or reducing severity of otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                  H. influenzae fimbrin peptide/T cell epitope chimaera LB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 94.3%; Score 99; DB 7; Length 40; Local Similarity 94.7%; Pred. No. 9.9e-10; nes 18; Conservative 0; Mismatches 1; Indels
                                                                                                                        Fimbrin, T cell epitope, vaccine, otitis media, auditory, antiinflammatory, LB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-typable Haemophilus influenza (NTHi) fimbrin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID NO 10; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR66294 standard; protein; 359 AA.
                                ADC89661 standard; peptide; 40 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSDYKFYBAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSDYKFYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                   19-AUG-2002; 2002US-00223711.
                                                                                                                                                                                                                                                                          98US-00148711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                   Kaumaya PTP;
                                                                              (first entry)
                                                                                                                                                          Chimeric.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                           (KAUM/) KAUMAYA P T P.
                                                                                                                                                                                                                                                                                               (BAKA/) BAKALETZ L O.
                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-810881/76.
                                                                                                                                                                                                      JS2003113344-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40 AA;
                                                                                                                                                                                  Measles virus.
                                                                                                                                                                                                                                                                          04-SEP-1998;
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25-MAR-2003
09-AUG-1995
                                                                                                                                                                                                                                                                                                                                  Bakaletz LO,
                                                                              01-JAN-2004
                                                                                                                                                                                                                             19-JUN-2003.
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                                                       ADC89661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
          RESULT 14
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IID AAR(
XX
AC AAR(
XX
DT 27-1
DT 25-1
DT 25-1
XX
XX
                      ADC89661
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The fimbrin proteins from 15 randomly selected type b and non- typable clinical isolates of Haemophilus influenzae share common epitopes. Thus frimbrin isolated from non-typable Haemophilus influenzae 1128 strain is a particularly suitable immunogen to protect against the different non-typable HJ. influenzae that cause otitis media. Fimbrin protein is sproduced by culturing a transformed microbial host., pref. E.coli, sporodoptera frugiperda or a mucosal pathogen. Fimbrin protein (FP) produced by this process is claimed. The FP protein migrates in polyacrylamide genes to a posn. equiv. to a mol. W. of 25.5 kD or 37.5 kD. (Updated on 25-MAR-2003 to correct PM field.) (Updated on 25-MAR-2003 to correct PM field.) (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine comprising non-typable Haemophilus influenza fimbrin protein -
useful in studying, preventing or reducing the severity of otitis media,
also fimbrin protein and DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Haemophilus influenzae; PS-IHke fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.3%; Score 99; DB 2; I 94.7%; Pred. No. 1.3e-08; iive 0; Mismatches 1;
                                                                                                                                              234. .249
/label= internal CNBr fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kolattukudy PE, Bakaletz LO, Sirakova T;
                                                                                            22. .33
/label= amino terminus
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                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (OHIS ) UNIV OHIO STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 5; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 RSDYKFYEDANGTRDHKKG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSDYKFYEAANGTRDHKKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 94.7
nes 18; Conservative
Haemophilus influenzae.
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N-PSDB; AAQ78916.
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antigenic P5-like fimbrin subunit peptides used in vaccines against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY19955 to AAX79993, and
                                                                                         The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAT79955 to AAT79933, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Haemophilus influenzae; PS-INke fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; ottiis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                                                                                                                                                                                                                                                          Score 96; DB 3; Length 19;
Pred. No. 1.4e-09;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lobet
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                                                                Example 1; Page 29; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY79963 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                                                             1 RSDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                           19
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           RSDYKFYDDANGTRDHKKG
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                                Haemophilus influenza.
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                                                                                                                                                                                                                                             the present invention
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                                                                                                                                                                                                                                                                             Sequence 19 AA;
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                  Novel
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                                                                                                                                                                                                                                                                                                          The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAV71955 to AAY7993, and AAX91201 to AAX91202, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                             antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein, Haemophilus influenzae, PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99; DB 3; Length 464;
Pred. No. 1.8e-08;
0; Mismatches 1; Indels
                                                                                                                                                             Lobet Y;
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                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS (OHIS ) UNIV OHIO STATE RES FOUND.
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                                                                                                                                                             Dequesne G,
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                                                                                                                                                                                                                                                                                             Claim 14; Fig 5; 68pp; English.
                                               99WO-US011980
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Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                                                                                                             Cohen J,
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N-PSDB; AAZ91252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 464 AA;
                                                                                                                                                            Bakaletz LO,
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                                               28-MAY-1999;
                                                                              11-JUN-1998;
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                16-DEC-1999
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                               Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; onjunctivitis; lower respiratory tract infection.
                                                                                                       Non-typeable H. influenzae group 1 LB1(f) peptide N152NP.
                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
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                           AAY79956 Btandard; peptide; 19
                                                                             (first entry)
                                                                                                                                                                                               Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                       Bakaletz LO,
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                                                   AAY79956;
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
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 AAZ91201 to AAZ91252, represent sequences used in the exemplification of
the present invention
                                                                                                                                                                                                                                                                                                               Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                 Length 19
                                                                                          1; Indels
                                                                 90.5%; Score 95; DB 3; 1
94.4%; Pred. No. 2.1e-09;
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Pred. No. 3.1e-09;
0; Mismatches 2;
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                                                                                          0; Mismatches
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                                                                                                                                                                                                            AAY79958 standard; peptide; 19 AA
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RSDYKFYEVANGTRDHKK 18
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                                                                            17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the present invention
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nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 AA;
                                       Sequence 19 AA;
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                                                                 Query Match
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Dequesne G,

Cohen J,

98GB-00012613.

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                                                                                   ofitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAX79993, and AAS91201 to AAZ91252, represent sequences used in the exemplification of the present invention
                                                                    aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-typable Haemophilus influenzae; fimbrin; T-cell epitope;
The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such
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                                                                                                                                                                                                                                                                                       Score 94; DB 3; I Pred. No. 3.1e-09;
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                                                                                                                                                                                                                                                                                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 1 RSDYKFYEAANGTRDHKKG 19
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                                                                                                                                                                                                                                                                                       89.5%;
89.5%;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Autibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY19955 to AAY19993, and AAX301201 to AAX21252, represent sequences used in the exemplification of the present invention
peptide is useful for treating a non-typable Haemophilus influenzae (NTH1) infection and otitis media. The synthetic peptides do not require tedious purification techniques. The present sequence represents the amino acid sequence of H. influenzae fimbrin subunit peptide #1.
                                                                                                                                                                                                                                                                                                                                                         Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Haemophilus influenzae; PS-Hike fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes antigenic P5-like fimbrin subunit peptides (LBI(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such prevention, and treatment of Haemophilus influenzae infections, such
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                                                                                                                                                                                                                                                                                                                                 Non-typeable H. influenzae group 1 LB1(f) peptide NTHI-601.
                                                                                              88.6%; Score 93; DB 6; Length 18; 94.4%; Pred. No. 4.4e-09; tive 0; Mismatches 1; Indels
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Pred. No. 1e-08;
1; Mismatches
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                                                                                                                                                      1 RSDYKFYEAANGTRDHKK 18
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88.9%;
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                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
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                                                                                                            Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                         The invention relates to the manufacture of a synthetic chimeric peptide comprising a non-typable Haemophilus influenzae fimbrin peptide fused via a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce an immune response against non-typable Haemophilus influenzae. This sequence represents an example of a H. influenzae fimbrin peptide used to generate the chimeric peptide
                                                                                                                                                                                                          Synthetic chimeric fimbrin peptide - useful for vaccination against non-
typable Haemophilus influenzae.
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Pred. No. 4.4e-09;
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ilarity 94.4%;
Conservative (
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                                                                                               02-JUN-1995;
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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Pred. No. 1.6e-08;
1; Mismatches 2; Indele
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                                                      Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAS91201 to AAAS91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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Pred. No. 1e-08;
1; Mismatches 1; Indels
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                                                                        AAY79968 standard; peptide; 19 AA
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RSDYKFYEEANGTRDHKR 18
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88.9%;
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Matches 16; Conservative
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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              otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
prevention, and treatment of Haemophilus influenzae infections, such as
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0; Mismatches 2; Indels
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                                                                                                                                                                                                                   1 RSDYKFYEAANGTRDHKK 18
                                                                                                                                                                                                                                                                                                                              AAY79962 standard; peptide; 19
                                                                                                                                                                                                                                              RSDYKLYEVANGTRDHKK 18
                                                                                                                                                   84.8%;
88.9%;
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Best Local Similarity
Matches 16; Conserv
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                                                                                         Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                          The present invention describes antigenic P5-like fimbrin subunit peptides (LBL(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAZ91201 to AAZ91222, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine, non-typeable Haemophilus influenzae, ntHi, infection, chimeric protein, Haemophilus influenzae, P5-like fimbrin protein, lipoprotein D, LB1(f); immunogenic, antigenic, otitis media, sinusitis, conjunctivitis, lower respiratory tract infection.
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Pred. No. 2.3e-08;
; Mismatches 2; Indels
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(OHIS ) UNIV OHIO STATE RES FOUND
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                                Dequesne
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84.2%;
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                              Cohen J,
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                                                                                                         Haemophilus influenza.
                                                            WPI; 2000-116457/10.
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                              Bakaletz
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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              Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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83.3%; Pred. No. 7.9e-08;
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(OHIS ) UNIV OHIO STATE RES FOIND
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Matches
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Haemophilus influenza.
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                                                                                                                                                                                                                                                                                                                                              Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Hamphilus influenzae; PS-like fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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84.2%; Pred. No. 3.5e-08;
ive 1; Mismatches 2; Indels
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                        1 RSDYKFYNDANGTRDHKK 18
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RSDYKFYEAANGTRDHKK
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nes 16, Conservative
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Haemophilus influenza.
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                                                                                                                            Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
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                                                                                                                                                                           The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Reemophilus influenzae infections, such
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Pred. No. 1.2e-07;
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                                                                                       Dequesne G,
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                                                                                                                                                         Disclosure; Page 46; 68pp; English
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84.2%;
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                                       98GB-00012613,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-00012613
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                       Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
                                                                                                          WPI; 2000-116457/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-116457/10
                                                                                                                                                                                                                                                                                       Sequence 19 AA;
                                                                                      Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9964067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1999;
                   28-MAY-1999;
                                       11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bakaletz LO,
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16-DEC-1999
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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                                                                                                                                                                                              Otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79933, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                              The present invention describes antigenic P5-like fimbrin subunit peptides (IBI(f) peptides) of F9-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-typeable H. influenzae group 1 LB1(f) peptide NTHI-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 85; DB 3; Length 12,
Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lobet Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
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Example 1; Page 29; 68pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY79969 standard; peptide; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKFYEDANGTRDRKTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.0%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 AA;
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us-09-719-379a-1.rag

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The invention relates to a synthetic chimaeric fimbrin peptide LB1 or LB2 comprises a first peptide unit derived from H. influenzae fimbrin, a second peptide unit containing a T cell epitope and a third linker peptide which connects the first peptide to the second. The chimaeric peptide which connects the first peptide to the second. The chimaeric peptide is useful for inducing an immune response in animals against non-typable Haemophilus influenzae (NTH1) and for preventing or reducing adherence of NTH1 to host cells thereby preventing or reducing the severity of ottis media. The present sequence is an H. influenzae fimbrin peptide for use in the chimaeric peptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                    Novel synthetic chimeric fimbrin peptide LB1 or LB2 comprising a first peptide unit, T cell epitope as second peptide unit and third linker peptide unit, useful for preventing or reducing severity of otitis media.
                                                                                                           Fimbrin; T cell epitope; vaccine; otitis media; auditory;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1; 15pp; English.
ADC89652 standard; peptide; 18 AA.
                                                                                H. influenzae fimbrin peptide #1.
                                                                                                                                                                                                                                                             98US-00148711
                                                                                                                                                                                                                                  19-AUG-2002; 2002US-00223711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSDYKFYEAANGTRDHKK
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                                                    (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 83.3
                                                                                                                                                Haemophilus influenzae.
                                                                                                                                                                                                                                                                                       (BAKA/) BAKALETZ L O.
(KAUM/) KAUMAYA P T P.
                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-810881/76.
                                                                                                                        antiinflammatory.
                                                                                                                                                                             US2003113344-A1.
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                                                      01-JAN-2004
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                           ADC89652;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   not identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nontypable H. influenzae HI outer membrane protein P5 was isolated by extraction of the outer membrane with detergents and cation-exchange chromatography. P5 (or its peptide fragments) are used in vaccines for prevention of H. influenzae infections implicated in otitis media, sinusitis and chronic pulmonary obstructive disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purified H.influenzae PS outer membrane protein - used for preventing reducing susceptibility to or treating H.influenzae infections.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                    P5 outer membrane protein; vaccine; otitis media; sinusitis; chronic pulmonary obstructive disease.
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                                      Score 84; DB 3; Length 19;
Pred. No. 1.8e-07;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                           /note= "amino acid at position 195 is
the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 7-8; 16pp; English.
                                                                                                                                                                                                                                                                          Nontypable H. influenzae P5 protein.
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                           AAR85450 standard; protein; 338
                                                                                              1 RSDYKFYEAANGTRDHKKG 19
                                                                                                           1 RSDYKFYEAANGTRDHKKG 19
                                     80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMCY ) AMERICAN CYANAMID CO
                                                                                                                                                                                                                                               (first entry)
                            Query Match
Best Local Similarity 78.9"
....hes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae.
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            Sequence 19
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                                Gaps
                                ö
Score 83; DB 7; Length 18;
Pred. No. 2.5e-07;
1; Mismatches 2; Indel8
                                                                                                                                                                                                                                                Non-typeable H. influenzae group 1 LB1(f) peptide N250NP.
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                                                                                                                                                            AAY79972 standard, peptide; 19
                                                             18
                                                                                       1 RSDYKFYEDLNGTRNHKK 18
    79.0%;
                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
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                                                                                                                                                               BX SX KK KK CBX BX YX YX ID
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RESULT 35 ADC89652

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9905-01304499-9905-01304499-9905-01304499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314819-9905-01314189-9905-01314199-9905-01314189-9905-013141819-9905-013141819-9905-013141819-9905-01314181819-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-013141818-9905-014033318-9905-01413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413328-9905-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-0144133338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-014413338-9005-0144133338-9005-0144133338-9005-014413338-9005-014413338-9005-014413338-9
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19-JUL-1999;
19-JUL-1999;
                  21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
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06-MAY-1999;
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11-MAY-1999;
14-MAY-1999;
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18-MAY-1999;
19-MAY-1999;
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08-JUN-1999;
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23-JUN-1999;
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28-MAY-1999
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18-JUN-19
18-JUN-19
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04 - JUN - 19
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21-JUN-1
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                                                                                                                                                                                                                                                                           Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                            The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                               Lobet Y;
                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                             Bakaletz LO, Cohen J, Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG45896 standard; protein; 311 AA
                                                                                                                                                                                                                                                                                                                                      Example 1; Page 29; 68pp; English
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                                                         99WO-US011980.
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Best Local Similarity 78.9
Matches 15; Conservative
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                                                         28-MAY-1999;
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                    16-DEC-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 10;
2; Mismatches
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Matches 9; Conservative
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A. Walley

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23-JUL-1999
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                                                                                                                                                                                                                               ced. No. 11;
Mismatches 7;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                            AAG20945 standard; protein; 361 AA
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990S-016070P
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nilarity 50.0%;
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9; Conserva
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                                                                                                    Length 361;
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                                                                                                    Score 48;
Pred. No.
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                                                                                                   Similarity 50.0%;
9; Conservative
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25-OCT-1999;
26-OCT-1999;
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086254 haemophilus
Q72bv4 desulfovibr
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089x84 arabidopsis
081789 arabidopsis
09fng6 arabidopsis
07pzh8 anopheles g
06ha27 trypanosoma
07yr14 rhinolophus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NTHI 1128;
MBDLINE=9422575; PubMed=7909539;
Sirakova T., Kolattukudy P.B., Murwin D., Billy J., Leake E., Lim D., Demaria T., Rakaletz L.;
"Role of fimbriae expressed by nontypeable Haemophilus influenzae in pathogenesis of and protection against otitis media and relatedness of the fimbria subunit to outer membrane protein A.";
Infect. Immun. 62:2002-2020(1994).
-I. FUNCTION: Acts as a fimbriae subunit.
-I. SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-I. SUBCELLULAR LOCATION: Integral membrane protein.
      Gaps
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InterPro; IPR006665; OmpA/Mot.
InterPro; IPR006665; OmpA/Mot.
InterPro; IPR006690; OmpA/Mot.
InterPro; IPR006690; OmpA_IIKE.
InterPro; IPR00699; OmpA_tmem.
Pfam; PF00691; OmpA; 1.
Pfam; PF001389; OmpA, membrane; 1.
PRINTS; PR01021; OMPADOMAIN.
PRINTS; PR01021; OMPADOMAIN.
PRODOM; PF001999; OmpA/Motes, 1.
PROSTITE; PS01068; OMPA; FALSE NEG.
Direct protein sequencing; Fimbria; Outer membrane; Porin; Signal;
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Pasteurellaceae; Haemophilus.
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94.3%; Score 99; DB 1; Length 359;
Best Local Similarity 94.7%; Pred. No. 3.2e-08;
Matches 18; Conservative 0; Mismatches 1; Indels
      1; Indels
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Outer membrane protein P5 precursor (OMP P5) (Fimbrin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By Bimilarity.
OmpA-like.
; 576BlC59B4818C37 CRC64;
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                                                                                                                                                                                                                                                                                                   359 AA
      0; Mismatches
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                                                                                                          1 RSDYKFYEAANGTRDHKKG 19
                                                                    1 RSDYKFYEAANGTRDHKKG 19
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22 359 Ou
332 344 By
278 322 Om
359 AA; 38340 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L08448; AAA24959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ompA; Synonyme=ompP5;
Haemophilus influenzae.
      18; Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
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ID OMS3 HAEIN
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DOMAIN
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      Matches
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Q76YV0
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                                                                                                             Bacteriophage Aehl.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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Viruses; deDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
NCBI_TaxID=227470;
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Petrov V., Nolan J., Bertrand C., Letarov A.V., Krisch H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petrov V., Nolan J., Bertrand C., Letarov A.V., Krisch H.M., Karam J.D.;
"Arramanas hydrophila phage Aehl complete genome.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.5%; Score 53; DB 2; Length 1211; 43.5%; Pred. No. 9.2;
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                                                                                                                                                                                                                                                                                                                                                                    Petrov V., Nolan J., Karam J.D.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY266303; AAQ17796.1; -.
Hypothetical protein.
SEQUENCE 1211 AA; 137634 MW; 6447E705BB2A9A88 CRC64;
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY266303; AAQ17796.1;
Hypothetical protein.
SEQUENCE 1211 AA; 137634 MW: 6447F70EBD330300
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                                                                                                                                                                                                                                                                            Karam J.D.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                 Last sequence update)
Last annotation update)
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5; Mismatches
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773 KNGFKFFNAENGKSISVRDHKQG 795
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086254;
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ID 08
AC 08
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Gaps

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47.6%; Score 50; DB 2; Length 536; 56.2%; Pred. No. 12; ive 2; Mismatches 5; Indela
                                                                                                                                                 536 AA; 59893 MW; C6D54A537BBCC286 CRC64;
                            TIGR; DVU1530; -.
InterPro; IPR001279; Blactmase-like.
InterPro; IPR011108; RMMBL.
                                                                                 Pfam; PF00753; Lactamase B; 1.
Pfam; PF07521; RMMBL; 1.
                                                                                                                                                                                                                                                                             2 SDYKFYEAANGTRDHK 17
  EMBL; AE017314; AAS96008.1;
TIGR; DVU1530; -.
                                                                                                                                                                                       Query Match
Best Local Similarity 56.2<sup>3</sup>
Matches 9; Conservative
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                                                                                                                       Complete proteome.
SEQUENCE 536 AA;
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Q9LN19;
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PubMed=1507118; DOI=10.1038/nbt959;
PubMed=1507118; DOI=10.1038/nbt959;
PubMed=1507118; DOI=10.1038/nbt959;
Rolonay J.F., Sebhadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Mard N.L., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullyvan S.A., Fourts D.E., Haft D.H., Sedlengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough.";
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Desulfovibrionaceae; Desulfovibrio.
NGII_TaxID=882;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Metallo-beta-lactamaes family protein.
OrderedLocusNames-DVUL530,
Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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                                                                                                                           Bacteria; Proceobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Outer membrane protein (Fragment).
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Pfam; PF01389; OmpA membrane; 1.
PRINTS; PR01021; OWFADOMAIN.
PRINTS; PR01022; OUTRWMBRANEA.
PRODOM; P0000930; OmpA/MocB; 1.
                                                                                                                                                                                                                                                         MEDLINE=99081716; PubMed=9864189;
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InterPro; IPR002369; OmpA/MotB.
InterPro; IPR006665; OmpA/MotB.
InterPro; IPR006699; OmPA_LIKE.
InterPro; IPR006498; OmpA_tmem.
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Matches 11; Conservative
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                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=740;
                                                                                                            Haemophilus sp.
                                                                                                                                                                                                                                     STRAIN=16N;
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SEQUENCE
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PubMed=15077118;

PubMed=15077118;

A Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,

Heidelberg J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M.,

A Kolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M.,

A Bugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,

Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,

A Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,

Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,

Relblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;

The genome sequence of the ansarobic, sulfate-reducing bacterium

Desulfovibrio vulgaris Hildenborough.";

Nat. Biotechnol. 22:554-559(2004).

R. Embl., ARS96088.1;

TIGR; DVUIS30;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
[1]
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Desulfovibrionaceae; Desulfovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                            Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
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Best Local Similarity 56.2%; Pred. No. 12;
Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536 AA; 59893 MW; C6D54A537BBCC286 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                               27-APR-2004 (TrEMBLrel. 27, Created)
27-APR-2004 (TrEMBLrel. 27, Last sequence update)
11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Metallo-beta-lactamase family protein.
                                                                                                                                                                            536 AA.
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                                                                                                                                                                            PRT;
206 ADYLFLESTYGDRDHK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| | |: | ||||
206 ADYLFLESTYGDRDHK 221
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Length 343;

5

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Hypothetical protein; Metal-binding; Zinc; Zinc-finger. SEQUENCE 343 AA; 38719 MW; E333D70369C31A83 CRC64;
                                                         Query Match
Best Local Similarity
''.a 9; Conserve
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les 9; Conserv
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Q8L789;
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--- SIMILARITY: Contains 1 RING-type zinc finger.

EMBL, 5020528; ARF97335.1; -...

HSSP; P38398; 1JM7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein At1g01350/F6F3_27.
Name=At1g01350/F6F3_27;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%; Score 48; DB 2; Length 304; 50.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                          GO; GO:000151; C:ubiquitin ligase complex; IEA.
GO; GO:000151; C:ubiquitin ligase complex; IEA.
GO; GO:0004842; F:nucleic acid binding; IEA.
GO; GO:0008270; F:rainc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
InterPro; IPR000571; Zif CCCH.
InterPro; IPR001841; Znf ring.
Pfam; PF00642; Zf-CCCH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7C107FA164251D27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWART; SMO0184; RING; 1.
SWART; SMO036; ZnP C3H1; 1.
PROSITE; PSO0518; ZF RING_1; UNKNOWN_1.
PROSITE; PS50089; ZF RING_2; 1.
Metal-binding; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00356; ZAF C341; 1.
PROSITE; PS00518; ZF RING 1; UNKNOWN 1.
PROSITE; PS50089; ZF RING 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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GO; GO: 0004842; F: ubiquitin-prot
GO; GO: 0008270; F: zinc ion bindi
GO; GO: 0016567; P: protein ubiqui
InterPro; IPRO00571; Znf CCCH:
Pfam; PF00097; Zf-CCH; I.
Pfam; PF00642; Zf-CCH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || || : :| || | |
151 SDEKLYKGIHGYTDHKAG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 AA; 34215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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SMART; SM00356; ZNF_C3H
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08GX84
1D Q8GX84
DT 01-M
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RA PALM CJUL AND SEQUENCE FROM N.A.

RA PALM CJU, Boweer L., Jones T., Banh J., Carninci P., Chen H.,

RA PALM CJU, Boweer L., Gones T., Banh J., Carninci P., Chen H.,

RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

RA Sakurai T., Sacu M., Seki M., Shinn P., Yamada K., Shinozaki K.,

RA Schrait. Theologis A., Davis R.W., Shinn P., Yamada K., Shinozaki K.,

BA Submitted (SEP-2002) to the EmBL/GenBank/DDBJ databases.

C -1 - SIMILARIY: Contains 1 RING-type zinc finger.

DR EMBL, AX136406; AAM97072.1; -.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

GO; GO:0000151; C:ubiquitin ligase activity; IEA.

DR GO; GO:0000151; C:ubiquitin pinding; IEA.

GO; GO:0000157; F:zinc ion binding; IEA.

DR GO; GO:000657; P:protein ubiquitination; IEA.

DR GO; GO:000571; Znf CCCH:

InterPro; IPR00057; Znf CCCH:

InterPro; IPR00184; RING; 1.

DR SMART; SM00184; RING; 1.

BR Pfam; PF00059; Zf-CCCH:

DR SMART; SM00184; RING; 1.

DR SMART; SM00186; ZF-RING; 1.

DR SMART; SM00186; ZF-RING; 1.

DR SMART; SM00186; ZF-RING; 1.

DR ROSITE; PS50089; ZF-RING; 1.

DR ROSITE; PS50089; ZF-RING; 1.

KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
Carninci P., Chen H., Cheuk R., Chan M.H., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hauan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,
Seki M., Shinn P., Tang C.C., Toroumi M., Wallender B.K., Wong C.,
Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,
Theologis A., Davis R.W.,
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                    PRT; 378 AA.
45.7%; Score 48; DB 50.0%; Pred. No. 16;
                                                                    2; Mismatches
                                                                                                                                                                                 Hypothetical protein At5g06420.
Name=At5g06420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 SDEKLYKGIHGYTDHKAG 203
                                                                                                                                     2 SDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SDYKFYEAANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 50.0%;
Conservative
                                                                    Conservative
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Gaps

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Trypanosoma brucei.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                           Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bastos I.M.D., Santana J.M., Grellier P.;
Submitted (JUL.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ96456; CAD42967.1;
InterPro; IPR001375; Peptidase S9.
InterPro; IPR001375; Peptidase S9.
InterPro; IPR001375; Peptidase S9.
InterPro; IPR001371; Peptidase S9.
InterPro; IPR001371; Pept S9.AS.
InterPro; IPR001371; Pept S9.AS.
InterPro; IPR001379; Ser_Setra.
IPRS PF001287; Peptidase S9; 1.
Pfam; PF001287; Peptidase S9; 1.
Pfam; PF002897; Peptidase S9 N; 1.
PRINTS; PR00862; PR0LIGOPTASE.
IPROSITE; PS00708; PROLIGOPTASE.
IPROSITE; PS00708; PROLIGOPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                      77111 MW; 97E9FDD34B130D02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          698 AA; 77597 MW; A969F75872E45910 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Prolyl oligopeptidase (EC 3.4.21.26).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       698 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.7%; Score 48; DB Best Local Similarity 50.0%; Pred. No. 34; Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Match
Local Similarity 43.5%; Pred. No. 43;
tes 10; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455
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                                                                                                                                                                                                                                          preliminary data.
EMBL; AABA010089886; BAA00289.1; -.
InterPro; IPR009613; DUT1222.
Pfam; PF06762; DUF1222; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: ||| :|:|||
TEQKFYNSADGTRIPMFIIHRKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |:|||:||
532 RFDFKFYDAAGSKSDAQK 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKFYEAANGTRDHKK 18
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(TrEMBLrel. 25, L
(TrEMBLrel. 25, L
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                                                                                                                                                                                                                                                                                                                                                                  678
                                                                                                                                                                                                                                                                                                                                                                                      678 AA;
                                               NCBI_TaxID=180454;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O7YR14;
01-OCT-2003 (
01-OCT-2003 (
01-OCT-2003 (
                                                                                                                          STRAIN=PEST
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NON TER
SEQUENCE
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                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
51-504 (TrEMBLrel. 27, Last annotation update)
51-304 (TrEMBLrel. 27, Last annotation update)
51-305-305 (TremBlook)
Arabidopsis thaliana (Mouse-ear cress)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicoryledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 5. II.
Sequence features of the regions of 1,044,062 bp covered by thirteen
physically assigned P1 clones.";
DNA Res. 4:291-300(1997).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-98069011; PubMed=9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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--- SIMILARITY: Contains 1 RING-type zinc finger.

EMBL, AB006700; BAD08964.1, --

EMBL, A0006710; BAD08964.1, --

GO; GO:0000151; C:ubiquitin ligase complex; IEA.

GO; GO:000157; F:ubiquitin ligase activity; IEA.

GO; GO:0008270; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:001567; P:zinc ion binding; IEA.

InterPro; IPR001841; Znf_CCCH.

Refam; PF00097; Zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%; Score 48; DB 2; Length 378; 50.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00184; RING; 1.
SWART; SM00184; RING; 1.
SWART; SM00186; ZnP C3H1; 1.
PROSITE; PS00618; ZF RING 1; UNKNOWN 1.
PROSITE; PS50089; ZF RING 2; 1.
Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 378 AA; 42460 MW; 173D71BBB8BA3FEZD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgCP9402 (Fragment).
Name-agCG54458; ORFNames=ENSANGG0000012855;
Anopheles gambiae str. PEST.
                                                 378 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22088475; PubMed=12093376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDEKLYKGIHGYTDHKAG 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0.
Best Aconservative
The State of Conservative
                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                               Tabata S.;
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                                                 O9FNG6
                                                                          Q9FNG6
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07PZH8
1D Q7PZH
DT 01-MA
DT 01-MA
DT 01-MA
DE AGCP9
GN NAMCE9
OS ANOPH
RESULT 11
Q9FNG6
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7

Gaps

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Indels

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304 RSQYKFTNAKVGKVGYRYGSGNRDNKK 330
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Q88325;
                                                                                   098879
                                                         RESULT 16
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                                                                                                                                                                                                                                                                                      Gaps
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Microchiroptera; Rhinolophidae;
Rhinolophinae; Rhinolophus.
                                                                                             MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An by Dylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AX243371; AAP50759.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S288c;
MEDLINE=97435481; PubMed=9290212;
Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
"Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical 39.6 kDa protein in GTR2-KRE11 intergenic region.
OrderedLocusNames=YGR165W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S64476; S64476.
Germonline; 141477; -.
SGD; S0003397; YGR1654.
GO; GO:0005763; C:mitochondrial small ribosomal subunit; IPI.
GO; GO:0003735; F:structural constituent of ribosome; IPI.
GO; GO:0009060; P:aerobic respiration; IEP.
GO; GO:0006412; P:protein biosynthesis; IC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
44.3%; Score 46.5; DB 1; Length 345;
Best Local Similarity 40.7%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 5; Indels 9
                                                                                                                                                                                                                                                      44.8%; Score 47; DB 2; Length 445; 69.2%; Pred. No. 32; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 345 AA; 39575 MW; 4E363E30F5056329 CRC64;
                                                                                                                                                                                                                             445 AA; 49395 MW; 6ECCAB23CB347E73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z72950; CAA97189.1; -.
                                                                                                                                                                                                                                                                                                                                        371 KLYSAATGTVDHK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast 13:1077-1090(1997).
                                                                                                                                                                                                                                                                                                               5 KFYEAANGTRDHK 17
                                                                                                                                                                                                                                                                      Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                 1445
 Rhinolophus creaghi.
                                                   NCBI_TaxID=178895;
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                               1445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome VII.
                                                                                                                                                                                  Lipoprotein.
NON TER
NON TER 44
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P53292;
                                                                                                                                                                                                                           SEQÜENCE
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YG3V_YEAST
ID YG3V_Y
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STRAIN=DG3000;
MCDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R GO; GO:0003674; C:nucleus; IEA.

R GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0006389; F:DNA-directed RNA polymerase activity; IEA.

R GO; GO:0006330; F:protein dimerization activity; IEA.

R GO; GO:0006330; F:protein dimerization activity; IEA.

R InterPro; IPR011261; RNAP dimeration.

R InterPro; IPR011262; RNAP INSTITE.

R InterPro; IPR011263; RNAP RB11-1ike.

R InterPro; IPR011263; RNAP RB11-1ike.

R InterPro; IPR011263; RNAP RB11-1ike.

R Pfam; PF01100; RNA_pol. D.

R Pfam; PF01100; RNA_pol. D.
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Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=21223349; PubMed=11323671;

Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng Wu X., Reith M., Cavalier-Smith T., Maier U.G.;

"The highly reduced genome of an enslaved algal nucleus.";

Nature 410:1091-1096(2001).

EMBL; AF093031; AAK39703.1;
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DNA-directed RNA polymerase; Nucleomorph.

RROHENCE 339 AA; 39207 MW; 5CDD56AC58F1A3CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 25, Last annotation update)
2-oxoglutarate dehydrogenase, E3 component, lipoamide
                                                                                                                                                                                                                                                                                                                                           Cryptophyta; Cryptomonadaceae; Guillardia.
                                                                                                   01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) DNA-directed RNA polymerase 40k chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.8%; Score 46; DB
43.8%; Pred. No. 35;
Live 4; Mismatches
339
                                                                           Created)
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                                                                                                                                                                                                                           Name=rpa5;
Guillardia theta (Cryptomonas phi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
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                                                                   01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-MAR-2004 (TrEMBLrel. 26,
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; C90126; C90126.
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ses 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=55529;
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                                                                                                                                                                                                                                                                                                           Nucleomorph.
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Gaps

6

1 RSDYKF-----YEAANGTRDHKK 18

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CG4064-PA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
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Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Belaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collmer A.; Schneider D.J., Tang X., The complete genome sequence of the Arabidopsis and tomato pathogen Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).

-! CATALYTIC ACTIVITY: Protein N(6)-(dihydrollpoyl)lysine + NAD(+) = protein N(6)-(lipoyl)lysine + NADH.

-! COFACTOR: Binds 1 FAD per subunit (By similarity).
                                                                                                                                                                                                                           (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engele R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selltrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
                                                                                                                                                                                                           -!- MISCELLANEOUS: The active site is a redox-active disulfide bond
                                                                                                                                                                                                                                                                 EMBL; AEG16603; AAO55717.1; -..

R HSSP; P14218; 1LPP.

R TIGR; PSPT02201; -..

GO; GO:00057301; -..

GO; GO:0001418; F:dihydrolipoyl dehydrogenase activity; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.

GO; GO:0006018; P:metal ion binding; IEA.

GO; GO:0006096; P:glycolysis; IEA.

R GO; GO:0006096; P:glycolysis; IEA.

R InterPro; IPR001327; FAD_Dyr_redox.

R InterPro; IPR001307; FAD_Dyr_redox.

R InterPro; IPR00100; Pyr_redox.

R InterPro; IPR00100; Pyr_redox.

R Pfam; PF00352; Pyr_redox.

R Pfam; PF00352; Pyr_redox.

R Pfam; PF00358; FR00945; HGNDTASE.

R PRINTS; PR00368; FADDPR.

R PRINTS; PR003189; FAD_Dyr_redox.

R PTGRPAM; PTGRPAMSE.

R PTGRPAM; PTGRPAMSE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00076; PYRIDÎNE REDÖX 1; 1.
Complete proteome; FAD; Flavoprotein; NAD; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 AA; 50026 MW; 912C9934A31D0505 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%; Score 46; 60.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                         oxidoreductase family.
1, AE016863; AAO55717.1; -.
9; P14218; 1LPF.
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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Matches 9, Conservative
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Name=NCU03250.1;
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O7SCQ3
AC 07SCQ
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RA Jaffe
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REDINES-20196006; PubMed=10731132;

REDINES-20196006; PubMed=10731132;

REDINES-20196006; PubMed=10731132;

REDINES-20196006; PubMed=10731132;

REDINES-20196006; PubMed=10731132;

REDINES-20196006; PubMed=10731132;

REDINES-20196006; Redines S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Evans Q., Chen L.X.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.H., Blazel R.G., Change M., Pfeiffer B.D.,

RA Bril J.F., Agbayani A., An H.J., Andrews-Prannkoch C., Bandwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

RA Ballew R.M., Basu D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Davies P., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugar M., Diaser S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Garlelian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Wernander J.R., Houck J.,

RA Harris N.L., Lei Y., Levitsky A.A., Liu Z., Liang Y., Lin X.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Mayn, Murphy B., Murphy L., Muzny D., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,

RA Melson D.R., Nelson K.A., Nixon K., Pacleb F., Pacleb J.M.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamvyssells M., Maucell E., Bielke C., Rudd S., Frishman D. Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Ogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                               Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%; Score 46; DB 2; Length 593; 75.0%; Pred. No. 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.

EMBL; AABXO1000066; EAA34529.1; -.
InterPro; IPR008266; Tyr pkinase AS.
PROSITE; PS00109; PROFIEIN KINASE TYR; UNKNOWN 1.
SEQUENCE 593 AA; 67688 WW; DB0893E77A4F8B7F CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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Matches 9; Conservative
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OrderedLocusNames=BT3565;
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MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12537568;
Medline S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patk S., Peiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finiahing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Whyers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Annotation of the Drosophila melanogaster euchromatic genome: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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FlyBase; FBgn0029808; CG4064.
SEQUENCE 670 AA; 75440 MW; AlF9A1BC297EEDDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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01-MAR-2004 (TrEMBLrel. 26, Last a
Putative TonB-dependent receptor.
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361 QAANGTRDH 369
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01-JUN-2003
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Q8A1U3
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE PEP! FAMILY OF MEMBRANE GLYCOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last amotation update)
Putative 125.2 kDa membrane glycoprotein in BIO3-HXT17 intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OrderedLocusNames=YNR065C; ORFNames=N3539;
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008959; CarboxypepD.reg.
InterPro; IPR00531; TonB receptor.
Pfam; PF00593; TonB dep.Rec; 1.
Complete proteome; Membrane; Outer membrane; Receptor; TonB box.
SEQUENCE 853 AA; 94509 MW; 311B270B87C760C1 CRC64;
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Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
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                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005215; F:transporte: activity; IEA.
GO; GO:0006810; P:transport; IEA.
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Germonline; 143410; -.
GGD; S0005348; YNR065C.
InterPro; IPR002860; Glyco hydro_BNR.
InterPro; IPR011040; Sialidase.
InterPro; IPR00581; VPS10.
Ffam; PP02012; BNR; 7.
SWART; SM00602; VPS10; 1.
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nes 9; Conservative
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                                                                                          NCBI_TaxID=818;
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P53751;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-SESSEG. / AB972;
MEDLINE-9731326; Pubmed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.,
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87(1997).
-I- SIMILARITY: BELONGS TO THE PEPI FAMILY OF MEMBRANE GLYCOPROTEINS.
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative membrane glycoprotein YIL173W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.
N-linked (GlcNAc. . .) (Potential).
Se MW; B2737747027B4B4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                    (Potential)
                                                                         (Potential) (Potential)
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                                                                                                                                            Score 46; DB 1; Length 1116;
Pred. No. 1.3e+02;
3; Mismatches 5; Indels
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Potential.
N-linked (GlCNAc. . .) (Potent N-linked N-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGD; SO001435; VTH.

GO; GO:0005768; C:endosome; IDA.

GO; GO:0006896; P:Golgi to vacuole transport; IMP.

InterPro; IPR002680; Glyco hydro_BNR.

InterPro; IPR001640; Sialidase.

InterPro; IPR005581; VPS10.
                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Putative membrane glycoprotein YIL173W precursor.
OrderedLocusNames=XIL173W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 1;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                      PRT; 1549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potential.
                                                                                                                                                                                                                                        3 DYKFYEAANGTRDHKKG 19
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                                                                                                                                            43.8%;
52.9%;
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52.9%;
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                                                                                                                              Query Match
Best Local Similarity 52.5-
Best Local 9; Conservative
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SMART; SM00602; VPS10;
957
336
336
553
846
985
934 95
35 33
336 33
553 55
846 84
985 98
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               RESULT 22
YIR3_YEAST
ID YIR3_YEAST
AC P40438;
                                  CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence, analysis of a 40.2 kb DNA fragment located near the left telomere of yeast chromosome X.";
Yeast 10:1657-1662(1994).
-!- SIMILARITY: BELONGS TO THE PEPI FAMILY OF MEMBRANE GLYCOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
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Potential.
N-linked (GlCNAc. . ) (Potential).
                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Putative membrane glycoprotein VJL22W precursor.
OrderedLocusNamee=YJL22W; ORFNames=J0213, HRC1549;
Baccharowyces crevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycotine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 1.9e+02;
3; Mismatches 5; Indels
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GermOnline; 141834;
SGD; SO003758; VTH2.
SGD; SO003758; VTH2.
InterPro; IPR012866; Glyco_hydro_BNR.
InterPro; IPR00581; VPS10.
InterPro; IPR00581; VPS10.
SMART; SM00602; VPS10; 2.
Glycoprotein; Hypothetical protein; Signal; Transmembrane.
SIGNAL
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                                                                                                                                                                                                                     PRT; 1549 AA.
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                                             || ||:|::||
DYNFYKASDGTCKLVKG 1306
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DYNFYKASDGTCKLVKG 1306
3 DYKFYEAANGTRDHKKG 19
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EMBL; Z49497; CAA89519.1; -.
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52.9%;
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                                                                                                                                                                                                                     STANDARD;
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SEQUENCE FROM N.A.
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Q7YQNS
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.

C STRAIN-ILS / ATCC 49652 / DSM 12025;

XRAIN-ILS / ATCC 49652 / DSM 12025;

MEDLINE-22103685; Pubmed=12039301; DOI=10.1073/pnas.132181499;

R Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,

Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,

A Holt I.E., Umayam L.A., Mason T.M., Whiteo O., Gruber T.M.,

Radune D., Vamathevan J.J., Khouril H.M., Whiteo O., Gruber T.M.,

Retchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic. anaeroble, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overcon Il L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D. W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Peldblyum T.V., Vang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Deterson J.J., Quackenbush J., Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.3%; Score 45.5; DB 2; Length 381; 62.5%; Pred. No. 48; ive 1; Mismatches 2; Indels 3
                                                                                                     Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
Chlorobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBa0057G07.1 (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buell R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome; Hypothetical protein.
SEQUENCE 381 AA; 42377 MW; 2CDDDEF72C48C479 CRC64;
                        01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Hypothetical protein CT2147.
OrderedLocusNames=CT2147;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=OSJNBa0057G07.1; Synonyms=OJ1365_D05.20;
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Matches 10; Conservative
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                                                                                                                                                                                NCBI_TaxID=1097;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OJ1365_D05.20.
OJ1365_D05.20.
Orza Sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae, Oryzeae, Oryza; Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II.L., Tsitrin T., Kim M.N., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V. Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 3 BAC OJ1365 D05 genomic sequence.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                   Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%; Score 45; DB 2; Length 274; 61.5%; Pred. No. 40;
                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
                                                EMBL; AC117988; AAP44689.1; -.
EMBL; AC096855; AAR87289.1; -.
Gramene; QYY1H0; -.
Hypothetical protein:
SEQUENCE 274 AA; 30566 MW; 5AA6364076740387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC096855; AAR87289.1; -.
Hypothetical protein.
SEQUENCE 274 AA; 30566 MW; 5AA6364076740387 CRC64;
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                                                                                                                                                                                                                   Score 45; DB 2
Pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Megaderma lyra (Indian false vampire).
                                                                                                                                                                                                                      42.9%;
                                                                                                                                                                                                                                                                                                                                                               | | |::|||| |
90 STYSFHDAANGNR 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STYSFHDAANGNR 102
                                                                                                                                                                                                                                                                                                                                2 SDYKFYEAANGTR 14
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                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Nipponbare;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39947;
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4 YKFY--EAANGTRDHK 17
                                                 Methanosarcina acetivorans.
    OrderedLocusNames=MA4384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 56.2
Matches 9; Conservative
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SEQUENCE FROM N.A.
STRAIN=bial niiA4;
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Q6XPR4
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    OOOCCOOOCCOOOCCOOOCCOOOCCOOOCCOOOCCOOOCCOOOCCOOOCCOOOCCOOOCCOOCCOOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCO
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STRAINERIND 2210633 / Serotype 03:K6;
MBDLINE-22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                 Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AF$48428; AAP$7384.1; --.
Mammalia; Eutheria; Chiroptera; Microchiroptera; Megadermatidae;
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Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.9%; Score 45; DB 2; Length 443; 69.2%; Pred. No. 69; tive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.9%; Score 45; DB 2; Length 449; Best Local Similarity 41.2%; Pred. No. 70; Matches 7; Conservative 5; Mismatches 5; Indels
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SEQUENCE 449 AA; 50016 MW; 323EC3B4732F5AE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 AA; 49385 MW; 4A77440E8FA69DFF CRC64;
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Hypotherical protein VP0238.
OrderedLocusNames=VP0238;
Vibrio parshames=VP0238;
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InterPro; IPR001279; Blactmase-like.
InterPro; IPR011108; RMMBL.
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                                                                                                                                                                                                                                              MEDLINE=22761261; PubMed=12878460;
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Pfam; PF07521; RMMBL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|| | |: | ::|:
195 RADYLFIESTYGNKEHE 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 KLYSAAAGTVDHK 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.2-
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                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                    NCBI_TaxID=9413;
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01-OCT-2003
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087T32
1D 087T3
AC 087T3
AC 087T3
DT 01-JT
DT 0
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Q8THX4
ID Q8THX
AC Q8THX
DT 01-JU
DT 01-OC
DE HYPOE
OCC OCC OX OX BRANK BRAN
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE A ATCC 35395 / DSM 2834;

STRAIN-C2A / ATCC 35395 / DSM 2834;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McBwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Limton L., McBwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McBwan P., McKernan K., Talamas J., Tirrell A., Sw I.,

RA Linton L., McBwan D.A., White O., White R.H., de Macario B.C.,

RA Springer T.A., Unwayam L.A., White O., White R.H., de Macario B.C.,

Rerry J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulsen I.T.,

RA Springer T.A., Unwayam L.A., White O., White R.H., Lander E.,

RA Ferry J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulsen I.T.,

RA The genome of Methanosacina acetivorans reveals extensive metabolic

RT and physiological diversity. ";

Genome Res. 12:512-542(2002).

RG GO:000080705; Frobalt ion binding; IEA.

GO: GO:000080705; Frobalt ion binding; IEA.

GO: GO:000080705; Frobalt in biosynthesis; IEA.

GO: GO:000086; P:methionine synthesis; IEA.

RG GO: GO:000086; P:methionine biosynthesis; IEA.

CO: GO:00008779; P:porphyrin biosynthesis; IEA.
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Burotiales; Trichocomaceae; Emericella.
NCBI TaxID=162425;
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"Analysis of the cred gene, a regulator of carbon catabolite
"repression in Aspergillus midulans.";
Mol. Cell. Biol. 11:5701-5709(1991).
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%; Score 45; DB 2; Length 631; 56.2%; Pred. No. 1e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Hypothetical protein.
SEQUENCE 631 AA; 68830 MW; AE0E5054F3FDD0CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Emericella nidulans (Aspergillus nidulans).
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InterPro; IPR011007; B12-binding.
InterPro; IPR001759; COMEL synth B12.
InterPro; IPR010988; M synth B12-like.
InterPro; IPR010257; Uro_decarbxyle.
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Pfam; PF02607; B12-binding_2; 1.
ProDom; PD003225; Uro_decarbxyls; 1.
                                          Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2214;
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MEDLINE=92017851; Pubmed=1922072;
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Query Match
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Matches
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Eurotiales; Trichocomaceae; Emericella.
NCPI_TaxID=162425;
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MCArthur A.G., Adam R.D., Aley S.B., Gillin Wartson H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia
                                                                                                                                         42.9%; Score 45; DB 2; Length 996; 36.8%; Pred. No. 1.7e+02; ive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%; Score 45; DB 2; Length 996; 36.8%; Pred. No. 1.7e+02; ive 6; Mismatches 6; Indels
Lockington R.A., Kelly J.M.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AZ1991-AAR02857.1; -.
InterPro; IPR004328; BRO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lockington R.A., Kelly J.M.;
"Brob from A. nidulans.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY21921; AAR02857.1; -.
                                                                          Pfam; PF03097; BRO1; 1.
SEQUENCE 996 AA; 110331 MW; 2DAC5DB796B2DBBB CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                        996 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-bial niiA4;
MEDLINE-92017851; PubMed=1922072;
Dowzer C.E., Kelly J.M.;
Analysis of the creA gene, a regulato
repression in Aspergillus nidulans.";
Mol. Cell. Biol. 11:5701-5709(1991).
                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                    206 QASYLYAQAIEGTQEHAKG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 QASYLYAQAIEGTQEHAKG 224
                                                                                                                                                                                                                            1 RSDYKFYEAANGTRDHKKG 19
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01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 36.8'
Conservative
                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                            Query Match
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Matches
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REDINE=2019006; PubMed=10731132;

RADARS M.D. Celniker S.E., Holt R.A., Boskins R.A., Galle R.F.,

Adams M.D. Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,

Adams M.D. Celniker S.E., Richards S., Ashburner W., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Bagu A., Baxter E.G., Helt G., Nelson C.R., Galbor G.L.,

RA Ballew R.M., Bagu A., Baxendale J., Bayraktaroglu L., Basaley B.M.,

Ballew R.M., Bagu A., Baxendale J., Bayraktaroglu L., Basaley B.M.,

Raberia C., Busam D.A., Buller H., Cadter B., Detter P., Chandra I.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RA Dodson K., Doup L.E., Downes M., Guzeriera S., Fleischmann W.,

RA Dodson K., Doup L.E., Downes M., Barris N.L., Harris M.C.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kaluush F., Karpen G.H., Ke Z., Kenlis On J.A.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., Morris J., Morny D.M.,

RA Balzolo M., Pittman G.S., Pan S., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Sampson M., Stenog R., Sun E.,

Shue B.C., Siden-Kiamos I., Sumpson M., Stenog R., Sun E.,

Spier E., Spradling A.C., Turner R., Wenissenbach J.,

Wang Z.Y., Wassarman D.A., Welley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Walliams S.M., Woodaget, Worley R., Welley W., Welsenbach J.,

Walliams S.M., Woodaget, Worley R., Wulley W., Welley W., We
                                                                                                                                               .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL; AACB01000006; EAA42440.1; -.
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Bukaryota, Metazoa, Arthropoda, Haxapoda; Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera, Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
-!- CAUTION: The sequence shown here is derived from an
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47.1%; Pred. No. 5.1e+02;
iive 3; Mismatches 6;
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1255 DYRTLNPSNGPRDSQKG 1271
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nes 8; Conserv
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RESULT 34
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
Yeh R.F., Zaverl J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                            MEDLINE=22426065; PubMed=12537568; Carlson J.W., Halpern A., Calniker S.E., Mheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finiabing a Wold-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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"Annotation of the Drosophila melanogaster euchromatic genome: a
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61.1%; Pred. No. 5.3e+02;
ive 2; Mismatches 3; Indels
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-1- SIMILARITY: Contains 1 LIM zinc-binding domain.
EMBL; AE003685; AAO41531.1; -.
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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PROSITE; PS60120; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS50023; LIM DOWAIN 2; 1.
LIM domain; Metal-binding; Zīnc.
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GO, GO:0007411, P:axon guidance; IMP.
InterPro; FR001715, Calponin-like.
InterPro; IPR001345; CytC, heme_BS.
InterPro; IPR001781; LIM.
                                                                                                                   Science 287:2185-2195(2000).
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Pfam; PF00412; LIM; 1.
ProDom; PD000094; LIM; 1.
SWART; SM00033; CH; 1.
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Terman J.R., Mao T., Pasterkamp R.J., Yu H.-H., Kolodkin A.L.;
"MICALs, a family of conserved flavoprotein oxidoreductases, function
in plexin-mediated axonal repulsion.";
Cell 0:0-0(2002).
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                                                                                                                                                                              Eukaryota, Metazoā, Arthropoda, Hēxapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Buyeryota; Bodopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Pred. No. 5.3e+02;
2; Mismatches 3; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF520713; AAM55242.1; -.
HSSP; P04006; 11ML.
FYBASe; FBGN0053208; MICAL.
GO; GO:0007411; P:axon guidance; IMP.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001715; Lalponin-like.
InterPro; IPR001781; LIM.
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Pfam; PF00412; LIM; 1.
SMART; SM0013; CH; 1.
PROSITE; PS50021; CH; 1.
PROSITE; PS50021; CH; 1.
PROSITE; PS50021; LIM DOMAIN 2; 1.
LIM domain; Metal-binding; Zinc.
  PRT; 2734 AA.
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                                               Created)
                                                                                                                                 Name=MICAL;
Drosophila melanogaster (Fruit fly)
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                                           01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
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Matches 11; Conservative
PRELIMINARY;
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                                                                                                              MICAL short isoform.
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Q8MUK0
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Gaps

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2537 RSDDESY--ANETREHKK 2552

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1 RSDYKFYEAANGTRDHKK 18

11; Conservative

Local Similarity

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42.9%; Score 45; DB 2; Length 3002; 61.1%; Pred. No. 5.9e+02; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                        PROSITE; PSS0021, CH; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
PROSITE; PS00190; LIM DOMAIN 2; 1.
LIM domain; Metal-binding; Zinc.
SEQUENCE 3002 AA; 332499 MW; 8C754C12F57E0337 CRC64;
         -!- SIMILARITY: Contains 1 LIM zinc-binding domain.
                                                                            GO; GO: 0007411; P: axon guidance; IMP.
InterPro; IPR001715; Calponin-like.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR011051; LIM.
InterPro; IPR011051; RmlC_like_cupin.
Pfam; PF00412; LIM; 1.
ProDom; PD000094; LIM; 1.
SMART; SM00132; LIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSDYKFYEAANGTRDHKK 18
                           EMBL; AE003685; AAO41532.1; -.
HSSP; PO4006; 11ML.
FlyBase; FBGN0053208; MICAL.
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Best Local Similarity 61.1%
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Pfam; PF00412; LIM; 1.
SMART; SM00033; CH; 1.
SMART; SM00132; LIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MICAL medium isoform.
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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burkok J., Brokktein P., Brottier P., Burtis K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Charler S., Domes M., Dagan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Angeler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Angelista C.C., Heinan T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Hewland T.J., Wei M.H., Ibegwam C., Jalai M., Kalush F., Karpen G.H., Kazi, K. Kanison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Kazi, C., Kanison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Wei M.H., Ibegwam C., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Martei B., McIntosh T.C., Morris J., McBherson D., Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A., Melson D.L., Martei B., Milahina N.V., Mobarry C., Morris J., Pacleb J.M., Ander D., Milahina W.V., Mobarry C., Morris J., Pacleb J.M., Ander D., Steniert K., Remington K., Saunders R.D., Scheeler F., Shen H., Shu B.C., Siden Krämes I., Simpson M., Strupski M., Wang A.H., Wang X., Shirb B.C., Shord W., Mulliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Walliams S.M., Woodager, Worley K.C., Wu D., Yang S., Zhu X., Smith H.O., Anden S., Pan R., Zaveri J.S., Zhan M., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Schence 287:2185-2195(2000).
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MEDLINE=22426070; PubMed=12537573;
MEDLINE=22426070; PubMed=12537573;
MEDLINE=22426070; Svirskas R.,
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker U.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schoceder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Terman J.R., Mao T., Pasterkamp R.J., Yu H.-H., Kolodkin A.L.;
"MICALS, a family of conserved flavoprotein oxidoreductases, function
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Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Eddopte-rygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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61.1%; Pred. No. 5.9e+02;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3002 AA; 332498 MW; FF3B9B44AF599346 CRC64;
                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I-SIMILARITY: Contains 1 LIM zinc-binding domain. EMBL; AF520714; AAM55243.1; -. HSSP; P04006; 1IML. FYBase; FBGR0053208; MICAL. GO; GO:0007411; P:axon guidance; IMP.
                                                                                                                                                     PRT; 3002 AA.
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PROSITE; PS60120; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS50023; LIM DOWAIN 2; 1.
LIM domain; Metal-binding; Zinc.
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InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR001781; LIM.
InterPro; IPR011051; RmlC_like_cupin.
                                                                                                                                                                                                     Created)
2805 RSDDESY--ANETREHKK 2820
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

to the EMBL/GenBank/DDBJ databases

Submitted (SEP-2002)

SEQUENCE FROM N.A.

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RAMMEDLINE=20196006, PubMed=10731132;

RAMMEDLINE=20196006, PubMed=10731132;

RAMMEDLINE=20196006, PubMed=10731132;

RAMMEDLINE=20196006, PubMed=10731132;

RAMMEDLINE=20196006, R.A. Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RAMMED R.C., Rogers Y.H., Blazel R.G., Champe M., Ffeiffer B.D.,

RAMMER, Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

RAMMER, Bandon R.C., Rogers Y.H., Blazel R.G., Champe M., Feiffer B.D.,

RAMMER, Bandon R., Baxendale J., Andrews-Pfannkoch C., Bador G.L.,

RAMMER, Benos P.V., Berner B.G., Helf G., Nelson C.R., Gabor G.L.,

RAMMER, Benos P.V., Berner B.P., Broketein P., Borchtar B.M.,

Ballew R.M., Banden M.R., Buck J., Broketein P., Borchtar B.M.,

Burkova D., Botchen M.R., Bouck J., Broketein P., Brottlar B.,

RAMMER, Cabliel B., Dollhe C., Davenpoort L.B., Davies P.,

RAMMER, Doup L.B., Downes M., Dugan Rocha S., Plaichmann W.,

RAMMER, Gabrielian A.E., Gasy N.S., Gelbart W.M., Glasser K.,

RAMMER, J., Houston K.A., Howland T.J., Hernandez J.R., Henckhann W.,

RAMMER, R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Alali M., Kalush F., Kalyen G.H., Ke Z., Kalp D., Lai Z.,

Lasko P., Lei Y., Leviteky A.A., Li J., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., Morphy D.M., Nalson D.L.,

RAMMER, M. Moy M., Murphy B., Murphy L., Murphy D.M., Nalson D.L.,

Ramer K.M., Moy M., Murphy B., Murphy L., Murphy D., Puri V., Resee M.G.,

Ramer K., Remington K., Saunders R., Dellard J., Puri, Wang X.,

Rhout S.M., Woodeger, Worley K.C., Wu D., Yang S., Yao Q.A., Yel R.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P.,

Rhenorn R., Woodeger, Worley K.C., Wu D., Yang S., Yao Q.A., Yel S.,

Rhenorn R., Moyers E.W., Wainstock G.M., Wainschen D.,

Wang Z.Y., Wassarman D.A., Wainstock G.M., Wainschen D.,

Wang Z.Y., Wassarman D.A., Wainstock G.M., Wainschen B.C.,

Richers R., Zhong W., Wainstock G.M., Vang S., Zhu X., Smith H.O.,

Rhenome R.C., Saden-Kiamos H., Wainstock G.M., Vang S., Zhu X., Smith H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celliker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finlshing a whole-genome seduence.", and the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name-MICAL, ORFRames-CG33208;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                               PRT; 4723 AA
                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426065; PubMed=12537568;
2805 RSDDESY--ANETREHKK 2820
                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CG33208-PC (Cg33208-pd)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
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                                                                                                                                                         RESULT 37
CASEBAL
DO COMPANY
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SEQUENCE FROM N.A

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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
MEDLINE=22426069; PubMed=12537572;
Misra S., Crobby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huany Y., Kaninker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                             Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00307; CH; 1.
Pfam; PF00412; LIM; 1.
Prodom; PF00013; LIM; 1.
SWART; SW00132; LIM; 1.
SWART; SW00132; LIM; 1.
PROSITE; PS0010; CH; 1.
PROSITE; PS0010; CYTCCHROME C; UNKNOWN 1.
PROSITE; PS00103; LIM DOMAIN 2; 1.
LIM domain; Mecal-binding; Zinc.
SEQUENCE 4723 AA; 525042 MW; C96ECC28393C7E9F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 LIM zinc-binding domain.
EMBL; AE003685; AAA041533.1; -.
HSSP; P04006; 11ML.
GO; GO:0007411; P:axon guidance; IMP.
InterPro; IPR001315; Calponin-like.
InterPro; IPR001345; CytC_heme_BS.
InterPro; IPR001361; LIM.
InterPro; IPR001051; RmlC_like_cupin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                         a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
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2; Mismatches
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MEDLINE=22426070; Pubmed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| : | || :|||
4526 RSDDESY--ANETREHKK 4541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26, MICAL long isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 61.1%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLYBASE
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Matches
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Q8MUJ8
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Q6PSK5;
                                                                                                                   QEPSKS
                          RESULT 40
Q6PSK5
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Terman J.R., Mao T., Pasterkamp R.J., Yu H.-H., Kolodkin A.L.;

"MICALs, a family of conserved flavoprotein oxidoreductases, function in plexin-mediated axonal repulsion.";

Cell 0:0-0(2002).

Cell 0:0-0(2002).

Cell 0:0-0(2002).

REMBLA PRESO15; AAM55244.1;

RHSSP: PO4006; LIML.

PlyBase; FBgn0053208; MICAL.

RICHERPO; IPR001715; Calponin-like.

InterPro; IPR001715; Calponin-like.

InterPro; IPR001715; RmlC_like.

InterPro; IPR001781; LiM.

RICHERPO; IPR001781; LiM.

RICHERPO; IPR001051; RmlC_like.cupin.

Pfam; PP00412; LIM; 1.

RP Probom; PD000094; LIM; 1.

RR SMART; SM00013; CH; 1.

RR SMART; SM00013; LIM; 1.
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Pasteurellaceae; Pasteurella.
NCBI_TaxID=47735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 42.9%; Score 45; DB 2; Length 4723; Local Similarity 61.1%; Pred. No. 9.9e+02; Pred. 11; Conservative 2; Mismatches 3; Indels
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STRAIN=PH252;

Bavies R.L., Lee I.;

Davies R.L., Lee I.;

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the ompA family.

RMBL; AYS82757; AAS91725.1;

InterPro; IPR006665; Bac_OmpA.

InterPro; IPR001388; OmpA/MotB.

InterPro; IPR001389; OmpA/motB.

Pfam; PF001899; OmpA, tnem.

Pfam; PF001891; OmpA, membrane; 1.

PRINTS; PR01022; OUTRWMBRANEA.

PRINTS; PR01022; OUTRWMBRANEA.

PFODOM; PD000930; OUTRWMBRANEA.

SEQUENCE 364 AA; 38662 MW; 83D13B28DAFF6D46 CRC64;
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PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
PROSITE; PS00129; LIM DOMAIN 2; 1.
LIM domain; Metal-binding; Zinc.
SEQUENCE 4723 AA; 524866 MW; 363EA40F9770B51A CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 364 AA
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42.4%; Score 44.5; I
Best Local Similarity 66.7%; Pred. No. 68;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4526 RSDDESY--ANETREHKK 4541
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138    RNDYKDY-YANGTKD 151
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Pasteurella trehalosi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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06 PSK1
AC Q6 PSK
AC Q6 PSK
AC Q6 PSK
DDT 05-JU
DDT 05-J
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                                                                                                       Name-ompA';
Pasteurella trehalosi.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 364;
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-PH146, and PH68;
Davies R.L., Lee I.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 364 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
42.4%; Score 44.5; D
Best Local Similarity 66.7%; Pred. No. 68;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the ompA family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November 24, 2004, 09:28:49 Job time : 90.3587 secs
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||| | ||||:|
138 RNDYKDY-YANGTKD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSDYKFYEAANGTRD 15
PRELIMINARY;
                                                                                                                                                                           NCBI_TaxID=47735;
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                               OM protein - protein search, using sw model
                         Copyright
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Run on:

November 24, 2004, 09:11:44 ; Search time 15.6957 Seconds (without alignments) 116.473 Million cell updates/sec

105 1 RSDYKFYEAANGTRDHKKG 19 US-09-719-379A-1 Perfect score: Sequence:

BLOSUM62 Scoring table:

283416 segs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	propable zinc fina	hypothetical prote		probable membrane	hypothetical prote	_	_	hypothetical prote	o	probable outer mem	putaive outer memb	hypothetical prote	secretory protein	probable iron-regu	conserved hypothet	S-receptor kinase	ď		hypothetical prote		u	S-locus-specific g	S-locus-specific g	conserved hypothet	glycogen synthase	t-complex protein	Fe-regulated prote	DNA topoisomerase	
Ü	G86143	S64476	C90126	863397	850705	D69429	T27959	T27958	S25329	E85729	D90888	G70157	\$27879	F81962	AI2747	831429	H97528	T00249	T23176	T15083	G84201	T14532	T14535	F82345	A81732	E90086	A56268	JC6552	CVBCD
DB	2	7	7	7	~	7	7	~	N	~	~	~	~	7	7	Н	7	7	~	~	~	~	~	~	~	~	~	~	-
* Query Match Length	304	345	339	1116	1549	308	634	863	1579	366	366	175	399	714	808	857	873	1353	109	129	142	426	429	455	474	519	713	1015	514
Query Match	45.7	44.3	43.8	43.8	43.8	41.9	41.0	41.0	41.0	40.5	40.5	40.0	40.0	40.0	40.0	40.0	40.0	40.0	39.0	σ		39.0		٠,	٠.	39.0	39.0	39.0	38.6
Score	48	46.5	46	46	46	44	43	43	43		42.5	42	42	42	42	42	42	42	41	41	41	41	41	41	41	41	41	41	40.5
Bult No.		7	m	4	ß	y	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	29

cardiolipin syntha prolyl oligopeptid prolyl oligopeptid prolyl oligopeptid diacylglycerol kin hypothetical prote hypothetical prote spoxide hydrolase-GGDEF family prote s-locus-specific g hypothetical prote hypothetical prote caseln kinasse I ho	88.6K hypotherical hypotherical prote
G82872 A37942 I38134 UG8760 T16301 F82348 F82348 T14574 T1418 T14918 T49616 S29521	C86406 T44153
01000000000000000000000000000000000000	100
233 244 25 25 25 25 25 25 25 25 25 25 25 25 25	786 903
	38.1
4444 0000 444444444 N N N O O O O O O O O O	44
0 H G W 4 B W W W W W 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 5

## ALIGNMENTS

probable zinc finger protein (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: GB6143
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hudres, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome of the plant Arabidopsis.
A;Title: Sequence and analysis of chromosome of the plant Arabidopsis.
A;Accession: G86143
A;Status: Proe: DNA
A;Accession: G96143
A;Status: Proe: DNA
A;Accession: Gabila

A;Cross-references: UNIPROT:Q9LN19; GB:AE005172; NID:g9665151; PIDN:AAF97335.1; GSPDB:GN:C;Genetics: A;Map position: 1 A; Residues: 1-304 <STO>

Gaps ö Length 304; 7; Indels Query Match
45.7%; Score 48; DB 2;
Best Local Similarity 50.0%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches

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RESULT 2

Nypothetical protein YGR165w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G7050
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64476
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
B;Rieger, to the Protein Sequence Database, May 1996
A;Reference number: S64071

A;Molecule type: DNA A;Residues: 1-345 KRIE> A;Cross-references: UNIRROT: P53292; EMBL: Z72950; NID:g1323289; PID:e243551; PID:g1323290 A;Experimental source: strain S288C

C,Genetics: A,Gene: MIPS:YGR165w A,Cross-references: SGD:S0003397

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hypothetical protein YJL222w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRC1549; hypothetical protein J0213; hypothetical C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S50705; S57012; S50354; S45150
R;Vandenbol, M.; Duzand, P.; Bolle, P.A.; Dion, C.; Portetelle, D.; Hilger, F.
                                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence analysis of a 40.2 kb DNA fragment located near the left telomere of ye
A;Reference number: S50701; MUID:95242842; PMID:7725802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1-1549 <VAN>
A,Residues: 1-1549 <VAN>
A,Cross-references: UNIPROT:P40890; EMBL:Z34098; NID:g496934; PIDN:CAA83988.1; PID:g4969-
A,Cross-references: UNIPROT:P40890; EMBL:A to the EMBL Data Library, June 1994
A,Nodes the nucleocide sequence was submitted to the Protein Sequence Database, R: submitted to the Protein Sequence Database, September 1995
A,Reference number: S56835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1549 <VAM>
A;Cross-references: BMBL:Z49497; NID:g1015614; PIDN:CAA89519.1; PID:g1015615; MIPS:YJL22:
R;Lye, G.; Bowman, S.; Churcher, C.
Submitted to the EMBL Data Library, December 1994
A;Reference number: S50349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1515,'L',1517-1549 <LYE>
A;Cross-references: GB:Z47047; EMBL:Z46921; NID:g603997; PID:g604002; GSPDB:GN00009; MIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CjAccession: D69429
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-308 «KLE>
A;Cross-references: UNIPROT:028835; GB:AE001004; GB:AE000782; NID:92689327; PIDN:AAB8981
C;Superfamily: [NiFe]-hydrogenase-3-type complex Eha, hydrophilic subunit EhaR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Species: Archaeoglobus fulgidus
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%; Score 46; DB 2; Length 1549; larity 52.9%; Pred. No. 45; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cikeywords: transmembrane protein
$2-18/00main: transmembrane #status predicted <TM1>
F;1374-1390/Domain: transmembrane #status predicted <TM2>
F;1423-1439/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AF1437 - Archaeoglobus fulgidus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1290 DYNFYKASDGTCKLVKG 1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: SGD: VTH2; MIPS: YIL173w
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les 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: S50705
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                                                                                                                                                                                                                                                                                                                                                      RESULT 3
C90126
DNA-directed RNA polymerase 40k chain [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C90126
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Residues: 1-339 <DOU>
A;Residues: 1-339 <DOU>
A;Residues: Leferences: UNIPROT:098879; GB:AF083031; NID:g13794326; PIDN:AAX39703.1; GSPDB:G;Genetics:
A;Gene: rpa5
A;Gene: rpa5
A;Map position: 3
A;Gene: nucleomorph
C;Superfamily: Saccharomyces cerevisiae DNA-directed RNA polymerase 40K chain
C;Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable membrane protein YNR065c - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein N3539
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63397
R;Dussterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D. submitted to the Protein Sequence Database, April 1996
A;Reference number: S6294
A;Accession: S63397
A;Cross-references: UNIPROT:P53751; EMBL:Z71680; NID:g1302593; PID:e239847; PID:g1302594
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YNR065c
A;Cross-references: SGD:S0005348
A;Accession: 14R
C;Keywords: transmembrane protein
F;941-957/Domain: transmembrane #status predicted <TML>
F;990-1006/Domain: transmembrane #status predicted <TML>
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                                                                 44.3%; Score 46.5; D
40.7%; Pred. No. 8.5;
ive 2; Mismatches
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43.8%; Score 46; DB
Best Local Similarity 43.8%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches
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Pred. No. 32;
3; Mismatches
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857 DYNFYKASDGTCKLVKG 873
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52.9%;
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Best Local Similarity
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A;Introns: 62/3; 125/3; 185/3; 211/3; 238/3; 286/2; 387/3; 440/3; 554/2; 703/1; 753/1; 78
                                                                                                                                                                                                                                                                                                                                                             carboxypeptidase Y-sorting protein PEP1 precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBL017c; protein YBL0302
C;Species: Saccharomyces cerevisiae
C;Species: 23-Apr-1993 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004
C;Accession: 825329; 845751; 84868
C;Accession: 825329; 845751; 84868
Yeast 8, 769-776, 1992
A;Attle. An 11.4 kb DNA segment on the left arm of yeast chromosome II carries the carbox a Management supplies that the carbox and the control number: 825329; WUID:93070614; PMID:1441754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-1579 <GOF>
A;Cross-references: EMBL:Z35778; NID:g536008; PIDN:CAA84836.1; PID:g536009; MIPS:YBL017c
A;Cross-references: EMBL:Z35778; NID:g536008; J.L.; Gharakhanlan, E.; Emr, S.D.
R;Marcusson, E.G.; Horazdovsky, B.F.; Cereghino, J.L.; Gharakhanlan, E.; Emr, S.D.
Cell 77, 579-586, 1994
A;Title: The sorting receptor for yeast vacuolar carboxypeptidase Y is encoded by the VP:
A;Teference number: S48868; MUID:94243924; PMID:8187177
A;Accession: S48868
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ViDescription: protein sorting of the soluble vacuolar carboxypeptidase Y is the soluble vacuolar carboxypeptidase Y is the sorting of the soluble vacuolar carboxypeptidase Y is worders a ATP; endoplasmic reticulum; glycoprotein; P-loop; purine nucleotide binding; 1-21/Domain: signal sequence #status predicted <SIG> 1,121/Domain: signal sequence #status predicted <SIG> 1,22-1579/Product: carboxypeptidase Y-sorting protein PEP1 #status predicted <MAT> 1,180-187/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1579 <VAN>
A;Cross-references: UNIPROT:P32319; EMBL:X68577; NID:g3302; PIDN:CAA48568.1; PID:g3303
A;Cross-references: UNIPROT:P32319; EMBL:X68577; NID:g3302; PIDN:CAA48568.1; PID:g3303
A;Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L.
Submitted to the Protein Sequence Database, August 1994
A;Reference number: S45745
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                                                                    Length 863;
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llarity 52.9%; Pred. No. 1.4e+02;
Conservative 2; Mismatches 6;
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Fils43-1567/Region: PEST sequence
Fils69-1579/Region: PEST sequence
Fils6/Binding site: ATP/GTP (Lys) #status predicted
                                                           Score 43; DB 2;
Pred. No. 77;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Gene: SGD:PEP1; VPS10; VPT1
;Cross-references: SGD:S0000113; MIPS:YBL017c
;Map position: 2L
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                                                              Query Match • ... 41.0%;
Best Local Similarity 50.0%;
Matches 7; Conservative
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251 FHELSNATRDYQPG 264
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Matches 9; Conserv
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A;Experimental source: clone ZK669
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A;Accession: T27974
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-634 <W12>
A;Residues: 1-634 <W12>
A;Cross-references: EMBL:246812; PIDN:CAA86848.1; GSPDB:GN00020; CESP:ZK669.1b
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A;Cross-references: EMBL:Z46812; PIDN:CAA86847.1; GSPDB:GN00020; CESP:ZK669.1a
A;Experimental source: clone ZK675
C;Genetics:
                                                                                                                                                                                                                           RESULT 7
T27959
hypothetical protein ZK669.1b - Caenorhabditis elegans
hypothetical protein ZK669.1b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27959; T27974
A;Thomas, K.
Submitted to the EMBL Data Library, September 1994
A;Feference number: Z20446
A;Accession: T27959
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Olecule type: DMA.
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Pred. No. 57;
4; Mismatches
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           ed. No. 19;
Mismatches
           Pred.
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        ilarity 72.7%;
Conservative
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Best Local Similarity 50.v.
7; Conservative
                                                                                                                                  210 SDYKMFEAARG 220
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     Best Local Similarity
Matches 8; Conserv
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A;Map position: 2
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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Conservative
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Best Local Similarity 53.33
Matches 8; Conservative
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Matches 7; Conserv
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nes 9; Conserv
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A, Molecule type: DNA
A, Residues: 1-714 < PAR>
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D90886
putaive outer membrane porin protein EC82076 [imported] - Escherichia coli (strain O157: C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Boll-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D90888
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8. 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90888
A;Accession: D90888
A;Residues: 1-366 <HAV>
A;Cross-references: UNIPROT:Q8XASO; GB:BA000007; PIDN:BAB35499.1; PID:gl3361542; GSPDB:G A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC82076
C;Superfamily: outer membrane protein phoE
                probable outer membrane porin protein Z2239 [imported] - Escherichia coli (strain O157:H C'Species: Escherichia coli BEST29 C'Accession: E85729 R'Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Title: Genome sequence of enterohemorrhagic Bscherichia coli O157:H7.
A;Title: Genome sequence strain O157:H7, substrain EDE933
C;Genetics:
A;Genetics:
A;Geneti
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dynotherical protein BB0464 - Lyme disease spirochete
hypotherical protein BB0464 - Lyme disease spirochete
c;Species: Borrella burgdorferi (Lyme disease spirochete)
c;Date: 13.Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: G70157
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
s Bowman, C.; Garland, S.; Pujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Atitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
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56.2%; Pred. No. 40;
ive 4; Mismatches
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80 DFKGYNDEANGSRDNK 95
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Matches 9; Conserv
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A;Molecule type: DNA
A;Residues: 1-175 «KLE»
A;Cross-treferences: UNIPROT:051420; GB:AE001151; GB:AE000783; NID:G2688371; PIDN:AAC6683
A;Experimental source: strain B31
C;Superfamily: Borrelia burgdorferi hypothetical protein BB0464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S27879
A;Molecule type: mRNA
A;Residues: 1-399 < CHA.
A;Cross-references: UNIPROT:035744; EMBL:M94584; NID:g202441; PIDN:AAB62394.1; PID:g20244
C;Superfamily: Streptomyces chitinase chi40
F;1-21/Domain: signal sequence #status predicted <SIG>F;1-2399/Product: secretory protein YM-1 #status predicted <MAT>
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: F81962
C;Accession: F81962
R;Parkhill, J; Achtuan, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Mature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
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A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable iron-regulated outer membrane protein NMA0453 [imported] - Neisseria meningitid:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004 C;Accession: $27879 R;Chang, N.C.A.; Liu, C.H.; Chang, N.C. Bubmitted to the EMBL Data Library, June 1992 abubmitted to the EMBL Data Library, June 1992 A;Description: Molecular characterization of a secretory protein (YM-1) transiently
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expre

us-09-719-379a-1.rpr

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hypothetical protein AGR_C_2573 [imported] - Agrobacterium tumefaciens (strain C58, Ceres C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Accession: H97528
R; Godoner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:Q8UFK4; GB:AE007869; PIDN:AAK87185.1; PID:g15156461; GSPDB:G:
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C;Accession: T00249

T;
Mursquothi, H.; Kamada, T.
Development 125, 3133-3141, 1998

A;Title: The ichl gene of the mushroom Coprinus cinereus is essential for pileus formati
A;Reference number: Z14131; MUID:98337832; PMID:9671586
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A;Residues: 1-1353 <MUR>
A;Cross-references: UNIPROT:074162; EMBL:AB012131; NID:g3551166; PIDN:BAA32788.1; PID:g3
A;Experimental source: strain 5302
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C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T2176
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    Length 857;
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Pred. No. 1.7e+02;
4; Mismatches 6; Indels
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Score 42; DB 1; Le
Pred. No. 1.1e+02;
3; Mismatches 5;
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Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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                                                                                                                                                                                                                                  210 EFYLLINGSPDHRSG 224
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 46.77
Best Local 7; Conservative
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A,Molecule type: DNA
A,Residues: 1-873 <KUR>
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                                                                Conserved hypothetical protein Atul393 [imported] - Agrobacterium tumefaciens (strain CS) Cybate: 11-Jan-2002 #text_change 09-Jul-2004 [c.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens [c.Species: Agrobacterium tumefaciens 11-Jan-2002 #text_change 09-Jul-2004 [c.Spacession: Al2747 [c.Spacession: Al2747 [c.Spacession: Al2747 [c.Spacession: Al2747 [c.Spacession: Al2747 [c.Spacession: A.2747 [
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A; Residues: 1-857 < OLD.>
A; Cross-references: UNIPROT: Q39393; EMBL: Z18921; NID: g17908; PIDN: CAA79355.1; PID: g17909
R; Kumar, V.; Trick, M.
A; Trick, M. 440-446, 1993
A; Title: Sequence complexity of the S receptor kinase gene family in Brassica.
A; Reference number: 839908; MUID: 94067027; PMID: 8246898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:QBUFK4; GB:AE008688; PIDN:AAL42399.1; PID:g17739809; GSPDB:
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                            MAINTIE: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CSB.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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F;658,662/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 42; DB 2; Length 809
46.7%; Pred. No. 1.1e+02;
tive 4; Mismatches 4; Indels
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A;Note: locus is highly polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics:
A,Gene: Atul393
A,Map position: circular chromosome
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781 SDHRFYDWKSGRFDH 795
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nes 7; Conservative
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A, Accession: $31429
A, Status: preliminary
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A;Residues: 559-708 <KUM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-809 < KUR>
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Rikusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:021842; EMBL:D85208; NID:92151147; PIDN:BAA21942.1; PID:9235
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross references: UNIPROT:023845; EMBL; D85211; NID:g2351153; PIDN:BAA21945.1; PID:g235 C; Superfamily: S-locus-specific glycoprotein homology C; Keywords: glycoprotein
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C;Species: Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                     S-locus-specific glycoprotein - wild cabbage (fragment)
NyAlternate names: S glycoprotein
C;Species: Barasica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14532
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C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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                                                          Length 142;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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7
                                                             Score 41; DB
Pred. No. 27;
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Best Local Similarity 46.7%; Pred. No. 81;
Matches 7; Conservative 3; Mismatches
                                                                                                               2; Mismatches
                                                                                                                                                                   1 RSDYKFYEAANGTRDHK 17
                                                                                                                                                                                                     69 RDEYDYVFEANGDRIHK 85
                                                             39.0%;
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202 EFYILVNGSRFHRSG 216
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                                                                                                                 8; Conservative
                                                             Query Match
Best Local Similarity
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A: Residues: 1-429 < KUS>
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        A;Gene: apa
                                                                                                               Matches
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G84201
diademosine tetraphosphate pyrophosphohydrolase [imported] - Halobacterium sp. NRC-1
C; Species: G2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Accession: G84201
R; NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84201
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <STO>
A;Coss.references: UNIPROT:Q9HS29; GB:AE004437; NID:g10580041; PIDN:AAG18979.1; GSPDB:GC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tisous to the control protein E03D2.2 - Caenorhabditis elegans
C, Special and Control protein E03D2.2 - Caenorhabditis elegans
C, Special and Control and Control and Control and C, Sep-1999 #text_change 09-Jul-2004
C, Accession: Tisous #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C, Accession: Tisous #sequence of C celegans cosmid E03D2.
A, Reference number: 218290
A, Reference number: 218290
A, Reference number: 218290
A, Accession: Tisous
A, Reference number: 218290
A, Experiments preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-129 <-RBC>
A, Cross-references: UNIPROT:044539; EMBL.AF039036; NID:g2736353; PIDN:AAB9
A, Experimental source: strain Bristol N2; clone E03D2
C, Genetics:
A, Gane: CESP:E03D2.2
A, Map position: 5
A, Introns: 19/1; 39/2; 90/2; 110/2
R;Dobson, R.
submitted to the EMBL Data Library, June 1996
A;Reference number: 219703
A;Accession: T23176
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Estiduse: 1-109 < WILD
A;Cross-references: UNIPROT:Q21089; EMBL:275543; PIDN:CAA99865.1; GSPDB:GN00023; CESP:KC
C;Genetics:
A;Gene: CESP:KO1D12.9
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                                                                                                                                                                                                                                                                                                                                                                                                          139.0%; Score 41; DB. 1arity 53.3%; Pred. No. 21; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.0%; Score 41; DB 53.3%; Pred. No. 25; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                   A;Map position: 5
A;Introns: 38/1
C;Superfamily: hypothetical protein K01D12.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RSDYKFYEAANGTRD 15
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Best Local Similarity 53.3.
Best Local 8; Conservative
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Matches 8; Conserv
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Gaps

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Length 519;

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A,Status: preliminary
A,Molecule type: DNA
A,Redidues: 1-713 <BEU>
A,Cross-references: UNIPROT:Q50944; GB:U13980; NID:g833694; PIDN:AAC43332.1; PID:g833695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog F;1-22/Domain: signal sequence #status predicted <SIG>F;62-191/Domain: tonB-dependent receptor amino-terminal homology <TNN>
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R;Zerwinski, R.M.; Lipniacki, A.; Staron, K.
R;Zerwinski, R.M.; Lipniacki, A.; Staron, K.
A;Title: CDNA cloning of Physarum polycephalum DNA topoisomerase I and expression analys A;Title: CDNA cloning of Physarum polycephalum DNA topoisomerase I and expression analys A;Reference number: JC6552; MUID:98245940; PMID:9583949
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A;Residues: 1-1015 <CZE>
A;Cross-references: UNIPROT:Q94705; GB:AF023910; GB:U63217; NID:g2642492; PIDN:AAC14193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA topoisomerase (EC 5.99.1.2) - slime mold (Physarum polycephalum)
N'Alternate names: emega-protein; micking-closing enzyme; type I DNA topoisc
C'Species: Physarum polycephalum
C'Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fe-regulated protein B precursor - Neisseria gonorrhoeae (strain FA19)
N;Alternate names: outer membrane protein FrpB
C;Species: Neisseria gonorrhoeae
C;Date: 13-Sep-1995 #sequence_revision 13-Sep-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Beucher, M.; Sparling, P.F.
J. Bacteriol. 76, 2041-2049, 1995
A;Title: Cloning, 804encing, and characterization of th A;Reference number: A56268; MUID:95238275; PMID:7721696
A;Accession: A56268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
39.0%; Score 41; DB 2; I
Best Local Similarity 47.4%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 8
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50.0%; Pred. No. 1.9e+02;
tive 2; Mismatches 6
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                                                                                               A;Genome: nucleomorph
C;Superfamily: molecular chaperone t-complex-type
C;Keywords: nucleomorph
                                                                                                                                                                                                             Score 41; DB 2
Pred. No. 99;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSDYKFYEAANGTRDHKKG 19
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                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          208 TDYTFYKKFNGT 219
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A56268
                                                                   A, Map position: 41
                                       A, Gene: tcpD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
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            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                    셤
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82245
R;Heidelberg, J.F.; Elsen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.;
R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD:20406833; PMID:10952301
A;Reference of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUD:20406833; PMID:10952301
A;Residues: 1-455 cHEI>
A;Residues: 1-455 cHEI>
A;Residues: 1-455 cHEI>
A;Residues: 1-456 cHEI>
A;Residues: 1-656 cHEI>
A;Reperimental source: serogroup O1; strain N16961; biotype El Tor
A;Genetics:
A;Genetics: A;Gene: VC0264
A;Map position: 1
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C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B90086
R;Douglas, S;Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
M;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUD:11323671; PMID:11323671
A;Recession: E90086
A;Status: preliminary
A;Residues: 1-519 <DOUS
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-474 <TET>
A;Residues: 1-474 <TET>
A;Cross-references: UNIPROT:Q9PLC3; GB:AE002285; GB:AE002160; NID:g7190212; PIDN:AAF3905
A;Experimental source: strain Nigg (MOPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Group synthase TC0181 [imported] - Chlamydia muridarum (strain Nigg)
C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: A81732
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.P.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Recession: A81732
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Pred. No.
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Pred. No.
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Best Local Similarity 38.9%;
Matches 7; Conservative 4
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A,Gene: TC0181
C,Superfamily: starch synthase
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Best Local Similarity 41.2
Matches 7; Conservative
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C.Accession: A77942
R.Rennex, D.; Hemmings, B.A.; Hofsteenge, J.; Stone, S.R.
R.Accession: A27942
R.Rennex, D.; Hemmings, B.A.; Hofsteenge, J.; Stone, S.R.
A.Title: CDNA cloning of pozcine brain prolyl endopeptidase and identification of the ac A;Reference number: A37942; MUID:91152034; PMID:1900195
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R. Vanhoof, G.; Goossens, F.; Hendriks, L.; De Meester, I.; Hendriks, D.; Vriend, G.; Van R. Vanhoof, G.; J63-366, 1994

A. Title: Cloning and sequence analysis of the gene encoding human lymphocyte prolyl endo: A.; Reference number: 138134; MUID:95047504; PMID:7959018
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N;Alternate names: proly1 endopeptidase
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                     projyl oligopeptidase (EC 3.4.21.26) - pig
N.Alternate names: prolyl endopeptidase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                    Gaps
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Pred. No. 1.6e+02;
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Pred. No. 1.6e+02;
4; Mismatches 3;
        50.0%; Pred. No. 1.2e+02;
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A;Molecule type: mRNA
                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||: |||: |||| SDYQTVQIFYPSKDGTKIPMFIVHKKG 459
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                                                                                                                                                                                                    241 RADYKFRSTIN-FRSHRK 257
                                                                                                                         1 RSDYKFYEAANGTRDHKK 18
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1 Similarity 40.7%;
11; Conservative
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Best Local Similarity 40.7%;
Matches 11; Conservative 4
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    Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-710 <REN>
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                                                                                                                                                                                                                         threonine synthase (EC 4.2.3.1) - yeast (Saccharomyces cerevisiae)

Nalterinate masses; protein YCRO53w
C.Species Saccharomyces cerevisiae
A;Recence muber: S22836, MUID:90371958; PMID:2204248
A;Recence muber: S22836, MUID:90371958; PMID:2204248
A;Recence number: S22836, MUID:90371958; PMID:2204248
A;Recence number: S20154, MUID:9017803; PMID:2408022
A;Title: Nucleotide sequence of the yeast THR4 gene encoding threonine synthase.
A;Recence number: S20154, MUID:9017803; PMID:2408022
A;Accession: S20154
A;Recence number: S20154, MUID:9017803; PMID:2408022
A;Crose-references: WRM:X7256; NID:94615, PIDN:CAA35157.1; PID:94616
A;Recence number: S19415
A;Recence number: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: G82872
A;Status: preliminary
A;Status: preliminary
A;Cuselucule type: DNA
A;Residues: 1-532 cGLA>
A;Cross-references: GB;AE002157; GB:AP222894; NID:g6899591; PIDN:AAF31002.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Genetic cls; UNS88
A;Genetic cls; UNS88
A;Genetic code: SGC3
C;Superfamily: cardiolipin synthase
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G82872
G82872
G82872
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G82882
G83882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.6%; Score 40.5; DB 1; Length 514; 53.3%; Pred. No. 1.2e+02; ive 3; Mismatches 3; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 532;
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                                               646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 YSFFQATNG-KDSKK 269
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||| | :| | :||
RSDMKKFEVARKLKDH
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Matches
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A;Residues: 1-319 <HEI>
A;Cross-references: UNIPROT:Q9KVB8; GB:AE004112; GB:AE003852; NID:g9654625; PIDN:AAF9340'
A;Experimental source: serogroup O1; strain N16961; blotype El Tor
                                                                                                                                                                                                                                                                                                                             RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T45731
Sylvate, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999
A;Reference number: Z233012
                                                                                                                                                                                                                       lypothetical protein VC0228 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
                                                                                                                                                                                                                                                  C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: F82348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epoxide hydrolase-like protein - Arabidopsis thaliana
N;Alternate names: protein F24M12.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 319;
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A;Molecule type: DNA
A;Residues: 1-323 <VIT>
A;Cross-references: UNIPROT:Q9SD45; EMBL:AL132980
A;Experimental source: cultivar Columbia; BAC clone F24M12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 1
C;Superfamily: Vibrio cholerae hypothetical protein VC0229
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GGDEF family protein - Deinococcus radiodurans (atrain R1)
C;Species: Déinococcus radiodurans
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Pred. No. 90;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB pred. No. 89; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 SDYDFKSTLSGKKQHK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.1%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SDYKFYEAANGTRDHK 17
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Best Local Similarity 53.8%;
Matches 7; Conservative
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266 YEGPNGTMEYVKG 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 3
A;Introns: 97/3; 157/3; 238/2
A;Note: F24M12.40
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                                                                              133 DYKCVEAANG 142
                          DYKFYEAANG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: DNA
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G186760

G186760

G186760

G186760

G186760

G2.5pecies: Lactococcus lactis subsp. lactis
C5.5pecies: Lactococcus lactis subsp. lactis
C5.5pecies: Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C5.Accession: G86760

G3.7 Mancker. P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
G600me Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A66625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: Î-218 «WIL»
A;Cross-references: UNIPROT:Q20147; EMBL:U40060; NID:g1055174; PID:g1055180; PIDN:AAA811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE005176; PID:g12724043; PIDN:AAK05185.1; GSPDB:d
                                              A; Molecule type: mRNA
A; Residues: 1-710 <705.
A; Residues: 1-710 <705.
A; Cross-references: UNIPROT: Q9XTA2; GB: AB028866; NID: g5103284; PIDN: BAA78907.1; PID: g510
A; Experimental source: brain
A; Note: in the authors' translation residues 124-129 and 130-172 are interchanged
C; Comment: This proline specific endopeptidase cleaves the peptide bond at the carboxyl
C; Superfamily: prolyl oligopeptidase
C; Keywords: hydrolase; serine proteinase
F; 554, 642, 680/Active site: Ser, Asp, His #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F38B6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Tales 1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16301
R;Wilcox, L.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F38B6.
A;Reference number: Z18491
A;Accession: T16301
                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                   38.6%; Score 40.5; DB 2; Length 710; 40.7%; Pred. No. 1.6e+02; tive 4; Mismatches 3; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 2; Length 151;
Pred. No. 42;
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C;Superfamily: Bacillus subtilis diacylglycerol kinase dgkA
C;Keywords: phosphotransferase
A; Reference number: JC5877; MUID: 98014979; PMID: 9353562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
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0; Mismatches
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433 SDYQTVQIFYPSKDGTKIPMFIVHKKG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SDYK----FYEAANGTR-----DHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Roeddues: 1-151 <STO>
A,CTOSB-references: UNIPROT:Q9CGK9; C
A,Experimental source: strain IL1403
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 SDYQFYMRAKRAKDMAAG 125
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A;Introns: 29/1; 54/1; 106/1; 135/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.1%;
ilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                             Local Similarity 40.7 nes 11; Conservative
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Best Local Similarity
Matches 8; Conserva
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Matches 8; Conserva
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                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Search completed: November 24, 2004, 09:30:12 Job time : 17.6957 secs
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C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C; Accession: E7526
R; White, 0.; Eigen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Venter, J.G.; Eraser, C.M.
S; Smith, H.O.; Venter, J.G.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Status: prellminary
A; Molecule type: DNA
A; Residues: 1.356 *WHI>
A; Residues: 1.356 *WHI>
A; Residues: 1.356 *WHI>
A; Residues: L.356 *WHI>
A; Residues: L.356 *WHI>
A; Residues: L.356 *WHI>
A; Cross-references: UNIPROT:Q9RRJ2; GB:AE002079; GB:AE000513; NID:g6460315; PIDN:AAF1204
A; Experimental source: strain R1
C; Genetics:
A; Gene: DR2498
A; Map posttion: 1
C; Superfamily: Stand-alone GGDEF protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 39
T14418
S-locus-specific glycoprotein - turnip (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Species: Brassica rapa (turnip)
C;Species: D'-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14418
C;Accession: T14418
C;Accession: T14418
C;Accession: T14418
C;Accession: T14418
C;Accession: T14418
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of class echanism.
A;Reference number: Z18078; MUID:97352858; PMID:9207151
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T14418
A;Restus: preliminary; translated from GB/EMBL/DDBJ
A;Restus: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNIPROT:023852; EMBL:D85218; NID:g2351167; PIDN:BAA21952.1; PID:g235
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 40
T49964
hypothetical protein US [imported] - human herpesvirus 6 (strain HST)
C;Decies: human herpesvirus 6
A;Variety: strain HST
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43964
R;Isegawa, Y: Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa J. Virol. 73, 8053-8063, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and A;Reference number: 22732; MUID:99412319; PMID:10482554
A;Reference number: 22732; MUID:99412319; PMID:10482554
A;Restus: preliminary; translated from GB/EMBL/DDBJ
A;Holecule type: DNA
A;Residues: 1-443 <1SE>
A;Cross-references: UNIPROT:Q9WT59; EMBL:AB021506; NID:g4995977; PIDN:BAA78225.1; PID:g4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.1%; Score 40; DB Best Local Similarity 46.7%; Pred. No. 99; Matches 7; Conservative 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| : |:| || || 339 RADERLYDAKNGGRN 353
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Gaps
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                                                                       Length 443;
                                                                       38.1%; Score 40; DB 2; Length 443
70.0%; Pred. No. 1.2e+02;
tive 1; Mismatches 2; Indels
A;Experimental source: strain HST; pop. variant C;Genetics:
A;Note: U5
                                                                       Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                               420 RDDYKYYEYA 429
                                                                                                                                            1 RSDYKFYEAA 10
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Sequence 128610, Sequence 120244, Sequence 120244, Sequence 20, Appl Sequence 205337, Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 3972, Appl Sequence 64039, A Sequence 125590, Sequence 160723, Sequence 159392, Sequence 1781, Appl Sequence 152876,

Sequence 3, Appli Sequence 7, Appli Sequence 162635,

Sequence 132021, Sequence 1172, Ap

Sequence 162635, Sequence 255389, Sequence 132021,

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GENERAL INFORMATION:

SEQUENCE 1, Application US/10203942

Publication No. US200096370A1

GENERAL INFORMATION:

APPLICANT: BERTHET, FRANCOIS-XAVIER

APPLICANT: BERTHET,

APPLICANT: PROGNAN, JON

APPLICANT: TOOLMAN, JON

TILLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE

TILLE OFFICIAL OUTER MEMBRANE

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US-10-739-930-10636

US-10-359-012-12

US-10-359-012-12

US-10-359-012-10

US-10-359-012-10

US-10-359-012-20

US-10-359-012-8

US-10-425-115-205237

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US-10-425-115-205237

US-10-425-115-205237

US-10-425-115-205318

US-10-425-115-25538

US-10-425-115-255318

US-10-425-115-255318

US-10-425-115-2255318

US-10-425-115-225711

US-10-425-39-152876

US-10-424-599-162635

US-10-424-599-162635

US-10-424-599-152318

US-10-424-599-152318
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94.3%; Score 99; DB 14;
Best Local Similarity 94.7%; Pred. No. 5.1e-09;
Matches 18; Conservative 0; Mismatches 1;
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Sequence 5, Appli
Sequence 10, Appli
Sequence 1, Appli
Sequence 19832,
Sequence 19832,
Sequence 4, Appli
Sequence 6986, A
Sequence 10635, A
Sequence 10635, A
Sequence 255044,
Sequence 255044,
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                                                                                                                                                    November 24, 2004, 09:29:11; Search time 71.663 Seconds (without alignments) 94.040 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PCT_RWW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_RWW PUB.pep:*
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-203-942-5
US-10-223-711-10
US-10-223-711-10
US-10-739-930-5878
US-10-437-96-130405
US-10-437-96-130405
US-10-282-122A-6986
US-10-282-122A-6986
US-10-739-930-10635
US-10-739-930-10635
US-10-359-012-19
US-10-437-963-142443
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                                                                                                                                                                                                                                                                                                                                                                                               1575965 seqs, 354694765 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                               protein search, using sw model
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105
1 RSDYKFYEAANGTRDHKKG 19
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Maximum DB seq length: 200000000
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Match Length DB
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Length 19;

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Indels

Length 18;

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Sequence 198352, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 10, 10, 10, 13, 10, 137, 963
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Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION:
FLIE REFERENCE: 38-21 (53377) B
CURRENT APPLICATION NUMBER: 10510/739,930
CURRENT APPLICATION NUMBER: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
LENGTH: 378
APPLICANT: Bakaletz, Lauren O.

APPLICANT: Kaumaya, Pravin T.P.

TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

FILE REFERENCE: 18525/04058

CURRENT APPLICATION NUMBER: 08/10/23,711

CURRENT APPLICATION NUMBER: 09/148,711

PRIOR APPLICATION NUMBER: 08/460,502

PRIOR APPLICATION NUMBER: 08/460,502

PRIOR APPLICATION NUMBER: 08/460,502

PRIOR SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

SEQ ID NO 110

FERROR FILE NOS NOS: 100

SEQ ID NO 100

FERROR FILE NOS NOS 100

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US-10-739-930-5878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.0%; Score 83; DB 14; L
Best Local Similarity 83.3%; Pred. No. 1.9e-06;
Matches 15; Conservative 1; Mismatches 2;
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Best Local Similarity 50.0%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches
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ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 SDEKLYKGIHGYTDHKAG 203
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JAPPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DENOEL, PHILIPPE
JAPPLICANT: PROJUMAN, JAN
JAPPLICANT: POOLMAN, JAN
JAPPLICANT: POOLMAN, JAN
JAPPLICANT: POOLMAN, JAN
JAPPLICANT: POOLMAN, JAN
JAPPLICANT: THONNARD, JOELLE
JITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
JITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT PELING DATE: 2002-08-15
JERIOR APPLICATION NUMBER: PCT/EP01/01556
JERIOR APPLICATION NUMBER: GB 0003502.2
JERIOR FILING DATE: 2001-02-15
JERIOR FILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.3%; Score 99; DB 14; Length 28; Best Local Similarity 94.7%; Pred. No. 7.6e-09; Matches 18; Conservative 0; Mismatches 1; Indels
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APPLICANT: Ramaya, Pravin T.P.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
FILE REFRENCE: 18525/04058
CURRENT APPLICATION NUMBRE: U5/10/223,711
CURRENT FILING DATE: 2002-08-19
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1998-09-04
PRIOR FILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 12
SEQ ID NOS: 12
SEQ ID NO 10
LENGTH: 40
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                                                 Sequence 5, Application US/10203942
Publication No. US20030096370A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10223711; Publication No. US20030113344A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Haemophilus influenzae US-10-203-942-5
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Best Local Similarity 94.7
Matches 18; Conservative
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
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NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                          Length 345;
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                                                                                                                                                                                                        44.3%; Score 46.5; D
40.7%; Pred. No. 38;
tive 2; Mismatches
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Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2001-02-09
                                                                                                                 TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Frawick, John
APPLICANT: Forsyth, R.
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PRIOR FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 345
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Best Local Similarity 40.7%
Matches 11; Conservative
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Best Local Similarity 60.0%
Matches 9; Conservative
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(5321)B
CURRENT APLICATION NUMBER: 02/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 130405
LENGTH: 114

TYPE: PP"
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                                                                                                                                                                                                                               Length 1226;
                                                                                                                                                                                                                             Query Match

44.8%; Score 47; DB 16; Length 12
Best Local Similarity 52.9%; Pred. No. 1.2e+02;
Matches 9; Conservative 3; Mismatches 5; Indels
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Publication No. US20040106173A1
GENERAL INFORMATION:
APPLICANT: Verde, Fulvia
APPLICANT: Verde, Fulvia
APPLICANT: Wiley, David J.
APPLICANT: Wiley, David J.
TITLE OF INVENTION: BOT1: Target for Antifungal Agents
FILE REFERENCE: 4052.24
CURRENT APPLICATION NUMBER: US/10/174,487
CURRENT FILING DATE: 2002-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_32570C.1.pep
US-10-437-963-130405
                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9401C.1.pep
US-10-437-963-198352
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 130405, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yihua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity 46.4%
                                                                                         TYPE: PRT
ORGANISM: Oryza Bativa
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LOCATION: (1)..(
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Sequence 142443.

Sequence 14263.

Sequence 14263.
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US-10-425-115-255044

j Sequence 255044, Application US/10425115

j Sequence 255044, Application US/10425115

j Sequence 255044, Application US/10425115

j GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yangwel
    APPLICANT: Cao, Yangwel
    TITLE OF INVENTION: Value
    APPLICANT: Cao, Yangwel
    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants
    TITLE OF SEPRENCE: 38-21 (53222)B
    CURRENT APPLICATION NUMBER: US/10/425,115
    NUMBER OF SEQ ID NOS: 369326
    SEQ ID NO 255044
    LENGTH: 220
    TUTLE OF US AROUSE ASSOCIATED WITH
    SEQ ID NO 255044
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US-10-437-963-142443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: MRT4577_164177C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%; Score 45; DB
42.1%; Pred. No. 41;
tive 3; Mismatches
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                                             ||| : | || ||:|||
5 RSDDESY--ANETREHKK 20
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90 STYSFHDAANGNR 102
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Matches 8; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
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US-10-437-963-142443
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Sequence 19, Application US/10359012

Publication No. US203022419A1

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

APPLICANT: TERMAN, John R.

APPLICANT: TERMAN, John R.

APPLICANT: MG, Tiany

APPLICANT: MG, Tiany

APPLICANT: TO HUNG-Heising

ITLE OF INVENTION: AND METHODS OF USING THE SAME

FILE REFERENCE: JU1840-3

TITLE OF INVENTION: AND METHODS OF USING THE SAME

FILE REPERENCE: J003-02-04

FILE REPERENCE: J003-02-04

FRIOR FILING DATE: 2002-06-13

PRIOR FILING DATE: 2002-06-13

PRIOR APPLICATION NUMBER: US 60/384,302

PRIOR PRILING DATE: 2002-06-30

PRIOR APPLICATION NUMBER: US 60/384,302

PRIOR PLING DATE: 2002-06-30

PRIOR PLING DATE: 2002-06-30

PRIOR PLING DATE: 2002-02-04

NUMBER OF SEQ ID NOS: 40

SOFFWARE: Patentin version 3.1

SEQ ID NO 19

LENGTH: 202

THENTH: 202
                                                                                                                                                              WG-10-739-930-10635
Sequence 10635, Application US/10739930
Sequence 10635, Application US/10739930
Sequence 10635, Application No. US20040216190A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53377) B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
SEQ ID NOS: 11088
SEQ ID NOS: 11088
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7
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US-10-739-930-10635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(168)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-359-012-19
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63 SSWKFYEAKNGFAVH 77
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US-10-359-012-19
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: TERMAN, Jon R.
APPLICANT: TERMAN, JON R.
APPLICANT: TERMAN, JON R.
APPLICANT: TERMAN, JON R.
APPLICANT: TALENAN, ROLA G.
APPLICANT: MAO TIANY
APPLICANT: WAD TIANY
APPLICANT: WINGHIANG
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: AND METHODS OF USING THE SAME
TITLE OF INVENTION: AND METHODS OF USING THE SAME
TITLE OF INVENTION: MOMBER: US 10/359,012
CURRENT APPLICATION NUMBER: US 60/384,302
PRIOR PLLING DATE: 2002-06-13
PRIOR PLLING DATE: 2002-05-30
PRIOR PLLING DATE: 2002-05-30
PRIOR PLLING DATE: 2002-05-30
PRIOR PLLING DATE: 2002-05-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PARCENT NESS: 40
SOFTWARE: PARCENT NESS: 40
SOFTWARE: PARCENT NESS: 40
SEQ ID NO 12
SEQ ID NO 12
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APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: ANOIST CALL APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
ITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ITLE OF INVENTION: 191321) B
CURRENT FILING DATE: 2003-05-14
CURRENT FILING DATE: 2003-05-14
SEQ ID NO: 204966
SEQ ID NO: 120244
LENGTH: 2932
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61.1%; Pred. No. 5.8e+02;
cive 2; Mismatches 3; Indels 2
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42.9%; Score 45; DB 16; Length 2932;
Best Local Similarity 61.5%; Pred. No. 6.3e+02;
Matches 8; Conservative 0; Mismatches 5; Indels
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US-10-437-963-120244
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Publication No. US20040123343A1
GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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US-10-359-012-12
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Best Local Similarity
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US-10-437-963-120244
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US-10-359-012-10
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APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION DOS: 2003-05-14
NUMBER OF SEQ ID NOS: 2004966
SEQ ID NO 128610
LENGTH: 1245
                                  Sequence 10636, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377) B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 10636
LENGTH: 320
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42.9%; Score 45; DB 16; Length 1245;
Best Local Similarity 61.5%; Pred. No. 2.5e+02;
Matches 8; Conservative 0; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 45; DB 17; Length 320;
42.1%; Pred. No. 61;
tive 3; Mismatches 8; Indels
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US-10-437-963-128610
                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C5473_3.p
US-10-739-930-10636
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NAME/KEY: unsure
LOCATION: (1)..(1245)
PERE INFORMATION: unsure at all Xaa locations
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 128610, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Buukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/10359012; Publication No. US20030232419A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Triticum aestivum
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Matches 8; Conservative
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US-10-437-963-128610
             -10-739-930-10636
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US-10-359-012-12
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GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: TERNAN, JOH R.

APPLICANT: TERNAN, JOH R.

APPLICANT: TERNAN, JOH R.

APPLICANT: TERNAN, JOH R.

APPLICANT: PASTERKAMP, Rohald J.

APPLICANT: WY, Hung-Haing

ITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT);

ITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REFERENCE: JHU1840-3

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: US 60/384,302

PRIOR APPLICATION NUMBER: US 60/384,302

PRIOR PILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-05-30

PRIOR PELING DATE: 2002-05-30

PRIOR POLICATION NUMBER: US 60/354,178

PRIOR PELING DATE: 2002-06-30

PRIOR PELING DATE: 2002-05-30

PRIOR PELING DATE: 2002-06-30

PRIOR PELING DATE: 2002-06-30
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APPLICANT: A Rosa, Thomas J.
APPLICANT: A Royalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plant Pack 13322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 205237
LENGTH: 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 14; Length 4723; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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Pred. No. 67;
1; Mismatches 1;
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; OTHER INFORMATION: Clone ID: MRT4577_118765C.1.pep
US-10-425-115-205237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
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                                                                           2805 RSDDESY--ANETREHKK 2820
                                                                                                                                                                                                                                                                                           Sequence 8, Application US/10359012 Publication No. US20030232419A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4526 RSDDESY--ANETREHKK 4541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKFYEAANGTRDHKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.4%;
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Best Local Similarity 61.1%;
Matches 11; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Drosophila
US-10-359-012-8
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                                                                                                                            APPLICANT: TOB COLORIN, Alex L.

APPLICANT: KOLODKIN, Alex L.

APPLICANT: TERMAN, Jon R.

APPLICANT: TERMAN, Jon R.

APPLICANT: TIANGY HASING THE SAME
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: MOLER: US 10/359,012
CURRENT APPLICATION NUMBER: US 60/389,325
PRIOR FILING DATE: 2002-06-13
PRIOR FILING DATE: 2002-05-30
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APPLICANT: TERMAN: JOR R.
APPLICANT: TERMAN: JOR R.
APPLICANT: TERMAN: JOR R.
APPLICANT: TERMAN: JOR R.
APPLICANT: MAO, Tianyi
APPLICANT: WI HUNG-Haiang
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: MOUBER: US 60/389,325
CURRENT FILING DATE: 2002-06-30
PRIOR FILING DATE: 2002-06-30
PRIOR FILING DATE: 2002-02-04
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 20
LENGTH: 3002
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; OTHER INFORMATION: CAL changed to W residues
US-10-359-012-20
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Publication No. US20030232419A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
                                                                                                         APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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61.1%; Pred. No. 6.4e+02;
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Sequence 10, Application US/10359012
Publication No. US20030232419A1
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ORGANISM: Artificial sequence
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Best Local Similarity 61.1
Matches 11, Conservative
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Matches 11; Conserva
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ORGANISM: Drosophila
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Sequence 20464, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: APPLICANT: APOUNT Thou, Yihua

APPLICANT: APPLICANT: Dou, Youla

APPLICANT: APPLICANT: Dou, Younger Cao, 
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; Publication No. US20030113161A1
; GENERAL INFORMATION:
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: 32132, A NOVEL FUCOSYLTRANSFERASE FAMILY
; TITLE OF INVENTION: 32132, A NOVEL FUCOSYLTRANSFERASE FAMILY
; TITLE OF INVENTION: 32132, A NOVEL FUCOSYLTRANSFERASE FAMILY
; TITLE OF INVENTION: 30132, A NOVEL FUCOSYLTRANSFERASE FAMILY
; TITLE OF INVENTION: 30132, A NOVEL FUCOSYLTRANSFERASE FAMILY
; TITLE OF INVENTION: 30132, A NOVEL FUCOSYLTRANSFERASE FAMILY
; FILE REPRENCE: 10440-046001
; CURRENT PAPLICATION NUMBER: US/09/844,948
; PRIOR APPLICATION NUMBER: US 60/200,604
; NUMBER OF SEQ ID NOS: 6
; SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.9%; Score 44; DB 17; Length 109; Best Local Similarity 47.4%; Pred. No. 29; Matches 9; Conservative 3; Mismatches 7; Indels
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41.9%; Score 44; DB 10; Length 292;
Best Local Similarity 53.3%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 5; Indels
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US-10-425-115-204064
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TYPE: PRT
ORGANISM: Zea mays
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US-10-184-648-22
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LENGTH: 292
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APPLICANT; Weyers in Such at B.
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APPLICANT: Liu, Yingdong
APPLICANT: Liu, Yihua
APPLICANT: Ehou, Yihua
APPLICANT: Scoren, Steven E
APPLICANT: Scoreen, Steven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53313)8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64039
LENGTH: 487
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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                               TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants FILE REPERBNERS: 38-77(52900)D
FILE REPERBNERS: 38-77(52900)D
CURRENT APPLICATION NUMBER: US,10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US,60/391,786
PRIOR PILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin Version 3.2
SEQ ID NO 1320
LENGTH: 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: LIB3245-500-B3_FLI.pep
US-10-425-114-64039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
41.4%; Score 43.5; DB 15;
Best Local Similarity 56.2%; Pred. No. 1.5e+02;
Matches 9; Conservative 3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-64039
Sequence 64039, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 YKFLEIVSGSTRNHKR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 YKFYEAANG-TRDHKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Sulfolobus tokodaii
US-10-389-566-1320
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269 YEAPHGLTRDHIKG 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-425-115-225538
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Publication No. US20040172684A1
Fublication No. US20040172684A1
Fublication No. US20040172684A1
Fublication No. US20040172684A1
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Covalic, David K.
APPLICANT: Covalic, David K.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 18-2153535 B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 39724
LENGTH: 337
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ilarity 53.3%; Pred. No. 94;
Conservative 1; Mismacches 6; Indele
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US-10-767-701-39724
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: PCT/US01/40607
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: PCT/US01/19543
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/802,872
PRIOR PILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR 22
LENGTH: 292
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; Sequence 1320, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 SKYKFYLAFENSKDH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| |: ||| |
274 RSDQALYDGGNGTTD 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conservat
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US-10-767-701-39724
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Length 68; Indels

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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 01516323318
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EBNGTH: 274
                                                                                                                                                                                                                                                                                                                                                        Sequence 50418, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)8

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

LENGTH: 154
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US-10-424-599-160723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: LIB3480-006-P1-K1-C5.pep
US-10-767-701-50418

, OTHER INFORMATION: Clone ID: MRT4577_137436C.1.pep
US-10-425-115-225711

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41.0%; Score 43; DB 15; L
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(154)
OTHER INFORMATION: unsure at all Xaa locations
                                                                 Query Match 41.0%; Score 43; DB Best Local Similarity 41.2%; Pred. No. 25; Matches 7; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 160723, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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52 SDTSIYRIRDGSRDHRQ 68
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FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(154)
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; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (5322)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 185590
LENGTH: 51
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; Sequence 225711, Application No. US20040214272A1
; Sequence 225711, Application No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Shou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REPERENCE: 38-21(53222)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 225711
; LENGTH: 68
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41.4%; Score 43.5; DB 17; Length 511;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 1
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US-10-425-115-185590
                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: MRT4577_137279C.1.pep
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 225538
LENGTH: 511
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293 YEAPHGLTRDHIKG 306
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                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
FEATURE:
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Sequence 128293, Application US/10437963
; Sequence 128293, Application US/10437963
; Sequence 128293, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brazauk, Brad
; APPLICANT: Bradauk, Brad
; APPLICANT: But Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128293
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APPLICANT: PILLUTLA, RENUKA
APPLICANT: BLOME, ARTHUR J.
APPLICANT: BLOME, ARTHUR J.
APPLICANT: SCHAFFER, LAUGE
APPLICANT: SCHAFFER, LAUGE
APPLICANT: SCHAFFER, JAKOB
APPLICANT: SCHAFFER, JAKOB
APPLICANT: OSTEKGAARD, SOREN
APPLICANT: ON UVBBER: US/09/962,756
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/538,038
PRIOR FILING DATE: 1998-002
NUMBER OF SEQ ID NOS: 2227
SOFTWARE: PERCENTIN VET: 2:1
SEQ ID NO 1781
LENGTH: 24
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US-09-962-756-1781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_30660C.1.pep
US-10-437-963-128293
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175 HKSCQREDGTDDHKKG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa
                                                                                                                                                                          US-10-437-963-128293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-962-756-1781
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brais, Verta
APPLICANT: Agenstrw, Petra
APPLICANT: Agenstrw, Pontus
APPLICANT: Agenstrw, Pontus
APPLICANT: Agenstrw, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI
FILE REFERENCE: L0461/7030
CURRENT APPLICATION NUMBER: US/10/17,980
CURRENT APPLICATION NUMBER: US/99/080,855
PRIOR APPLICATION NUMBER: 08/905.583
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13

"MONTAL ADDITION OF THE ADDI
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AROUND SON USING K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 159392
LENGTH: 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%; Score 43; DB 15; Length 442; 50.0%; Pred. No. 1.8e+02; Live 3; Mismatches 5; Indels
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US-10-424-599-159392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(442)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                           ; Sequence 13, Application US/10177980; Publication No. US20030166232A1; GENERAL INFORMATION:
                                             172 HKSCQKEDGTDDHKKG 187
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250 FHELSNATRDYQPG 263
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Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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40.5%; Score 42.5; DB 15; 50.0%; Pred. No. 34;
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40.0%; Score 42; DB 3
Best Local Similarity 87.5%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches
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                                                                                      3 DYK-FYEA-----ANGTRDHK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine max
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US-10-253-493-1781
Sequence 1781, Application US/10253493
Fublication No. US20040023887A1
GENERAL INFORMATION:
TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
FILLE REFERENCE: 1878-4056
CURRENT APPLICATION NUMBER: US/10/253,493
FRIOR APPLICATION NUMBER: 09/962,756
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1998-09-02
NUMBER OF SEQ ID NOS: 2227
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1781
LENGTH: 24
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                                                                                                                                                                                                                       Sequence 1781, Application US/10253471
| Publication No. US20030236190A1
| GENERAL INFORMATION:
| APPLICAT': PILLUTLA, |
| TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
| FILLE REPRESENCE: 1980-4057 |
| CURRENT APPLICATION NUMBER: US/10/253,471 |
| CURRENT PILING DATE: 2002-09-24 |
| PRIOR PILING DATE: 2000-09-24 |
| PRIOR PILING DATE: 2000-09-24 |
| PRIOR PILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR PILING DATE: 1909-09-22 |
| PRIOR PILING DATE: 1908-09-02 |
| NUMBER OF SEQ ID NOS: 2227 |
| SEQ ID NO 1781 |
| LENGTH: 24 |
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                                                Gaps
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US-10-253-471-1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
US-10-253-493-1781
                                              9
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      Length 24;
                                              Indels
                                              .;
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        DB 10;
      40.5%; Score 42.5; D
50.0%; Pred. No. 10;
iive 1; Mismatches
                                                                                      3 DYK-FYEA-----ANGTRDHK 17
                                                                                                             3 DYK-FYEA-----ANGTRDHK 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
query Match
Best Local Similarity 50.0
Matches 12; Conservative
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US-10-424-599-152876

i) Sequence 152876, Application US/10424599

i) Publication No. US20040031072A1

i) GENERAL INFORMATION:

i) APPLICANT: La Rosa Thomas J

i) APPLICANT: Cao Yongwel

i) APPLICANT: Cao Yongwel

i) APPLICANT: Cao Yongwel

i) TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

i) TITLE OF INVENTION: Dlants and Uses Thereof for Plant Improvement

i) FILE REPERENCE: 38-21 (53233) B

i) CURRENT PILING DATE: 2003-04-28

i) NUMBER OF SEQ ID NOS: 285684

i) SEQ ID NO 152876

LENGTH: 75
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Sequence 3, Application US/20203096370A1
Sequence 3, Application No. US2030096370A1
GENERAL INFORMATION:
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DENORIL, PHILIPPE
TITLE OF INVENTION: HARMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION UNMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: CB 0003502.2
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 13
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  Length 24;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_109070C.1.pep
US-10-424-599-152876
DB 15;
Score 42.5; D
Pred. No. 10;
1; Mismatches
Query Match
Best Local Similarity 50.0%;
Matches 12/3(Conservative
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1 RSDYKFYD 8

Search completed: November 24, 2004, 10:00:11 Job time : 72.663 secs

50418, A 160723, 39724, A 128293, 162795, 285321,

Sequence Sequence Sequence Sequence

3, Appli 7, Appli 204064,

US-10-425-114-68661 US-10-425-115-287966 US-10-425-115-287966 US-10-425-115-287946 US-10-425-115-287946 US-10-359-012-10 US-10-359-012-10 US-10-359-012-10 US-10-424-599-170099 US-10-424-599-170099 US-10-424-599-170099 US-10-203-942-3 US-10-203-942-3 US-10-203-942-3 US-10-424-115-204064 US-10-425-115-204064 US-10-425-115-204064 US-10-425-115-204064 US-10-425-115-204064 US-10-425-115-204064 US-10-425-115-204064 US-10-424-599-162793 US-10-424-599-162793 US-10-424-599-162793 US-10-424-599-16393 US-10-424-599-15993 US-10-424-599-15993 US-10-424-599-15993 US-10-424-599-15993 US-10-424-599-15993 US-10-444-599-15993 US-10-444-599-1599

Sequence Sequence Sequence

120244, 283230, 143107,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence I

135, App 54860, A 19648, A 159392,

Sequence Sequence Sequence Sequence Sequence

ALIGNMENTS

6568, Ap 272502,

Sequence Sequence Sequence Sequence

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42.5
42.5
Sequence 1, Appli
Sequence 5, Appli
Sequence 10, Appl
Sequence 205237,
Sequence 41199, A
Sequence 51811, A
Sequence 76, Appl
Sequence 75, Appl
Sequence 72279, A
Sequence 152876,
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                             ; Search time 71.663 Seconds (without alignments) 94.040 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_RNEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_RNEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_RNEW PUB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/USO7_RNEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_RNEW PUB.pep:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-203-942-5

US-10-223-711-10

US-10-425-115-205237

US-10-767-701-44199

US-10-767-701-51811

US-10-146-473-76

US-10-282-122A-72279

US-10-282-122A-72279

US-10-174-48-4

US-10-174-48-4
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                                                                                                                                                                                                                                                                                                                                                1575965 segs, 354694765 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                               November 24, 2004, 09:29:11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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107
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Match Length
                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                        Scoring table:
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                                                                                           OM protein
                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                 Run on:
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| Sequence | Application US/10203942 |
| Sequence | Application US/2003006370A1 |
| Publication No. US20030096370A1 |
| Publication No. US20030096370A1 |
| GENERAL INFORMATION: PRANCOIS-XAVIER |
| APPLICANT: BERTHET; FRANCOIS-XAVIER |
| APPLICANT: POOLMAN, JAN |
| APPLICANT: TOOLMAN, JAN |
| APPLICANT: TOOLMAN, JAN |
| APPLICANT: TOOLMAN, JAN |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCE |
| TITLE OF INVENTION: HAEMOPHILUS INFLUENCE |
| PRIOR APPLICATION NUMBER: US 0003502.2 |
| PRIOR FILING DATE: 2000-02-15 |
| NUMBER OF SEQ ID NOS: 9 |
| SEQ ID NO 1 |
| LENGTH 19 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Haemophilus influenzae
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RESULT

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                                                                                                                  JOHNSTON IN CORFIDENT IN CONTRACTORS APPLICANT: DERVIER, PRANCOIS-XAVIER APPLICANT: DERVOEL, PHILIPPE APPLICANT: DERVOEL, PHILIPPE APPLICANT: DERVOEL, PHILIPPE APPLICANT: POOLMAN, JAN 17 TOLD OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE ITILE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION FILE REFERENCE: B45210 CURRENT APPLICATION NUMBER: US/10/203,942 CURRENT FILING DATE: 2002-08-115 PRIOR APPLICATION NUMBER: CT/FEP01/01556 PRIOR PELING DATE: 2001-02-13 PRIOR PELLING DATE: 2000-02-15 NUMBER OF SEQ ID NOS: 9 SEQ ID NOS: 9 SEQ ID NO 5 SEQ ID
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Publication No US20030113344A1

GENERAL INFORMATION:

APPLICANT: Bataletz, Lauren O.

APPLICANT: Raumaya, Pravin T.P.

TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides

FILE REFERENCE: 18225/04058

CURRENT FILING DATE: 2002-08-19

FRIOR APPLICATION NUMBER: 09/148,711

PRIOR FILING DATE: 1998-09-04

PRIOR FILING DATE: 1998-06-02

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 10

LENGTH: 40
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100.0%; Score 107; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 19; Conservative 0; Mismatches 0;
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US-10-223-711-10
Sequence 5, Application US/10203942
Publication No. US20030096370A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RSDYKFYEDANGTRDHKKG 19
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Best Local Similarity 100.0
Matches 19, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-10-223-711-10
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US-10-223-711-1
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Sequence 20537, Application US/10425115
Publication No. US20040214272A1
GENERAL INCRNATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exoalic, David K.
APPLICANT: Thou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yinua
APPLICANT: Chou
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APPLICANT: Bakaletz, Lauren O.
APPLICANT: Kaumaya, Pravin T.P.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
CURRENT APPLICATION NUMBER: US/10/23,711
CURRENT APPLICATION NUMBER: US/10/23,711
FRIOR APPLICATION NUMBER: 09/148,711
PRIOR FILING DATE: 1998-09-04
PRIOR PILING DATE: 1995-06-02
RIOR PILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Version 3.1
SEQ ID NO 1
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US-10-425-115-205237
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Pred. No. 7.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Haemophilus influenzae US-10-223-711-1
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Best Local Similarity 84.6%;
Matches 11; Conservative
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126 SDYDEFYEDANGT 138
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Sequence 5878, Application US/10739930
Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT COVALIC, David K.
TITLE OF INVENTION:
PILE REFERENCE: 38-21 (53377) B
CURRENT APPLICATION NUMBER: 1067-108
CURRENT APPLICATION NUMBER: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
LENGTH: 378
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APPLICANT: Yamanoto. Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.0348
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                               Gaps
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43.9%; Score 47; DB 17; Length 378;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 9; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: ARATH-23APR03-C17092_1.p
US-10-739-930-5878
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LOCATION: (292) .. (292)
OTHER INFORMATION: X = any amino acid
                                                                     FEATURE:
NAME/KEY: UNSURE
LOCATION: (355)...(355)
COTHER INFORMATION: X = any amino acid
US-10-146-473-76
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FRICA PAPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Yeakind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Garr, Grant
APPLICANT: Fawick, Sobert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Arabidopsis thaliana
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207 SDYRFLEDVARTADH 221
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                                                                                                                                                                                                                                                                                                                                                                      Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Sequence 51811, Application US/10767701
| Publication No. US20040172684A1
| GENERAL INFORMATION:
| APPLICANT: Kovalic, David K.
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
| TITLE OF INVENTION WIMMER: US/10/767,701
| CURRENT APPLICATION WIMMER: US/10/767,701
| WUMBER OF SEQ ID NOS: 63128
| SEQ ID NO 51811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                      <del>.</del>;
                                                                                                                                                                                                                                                                                  Score 49.5; DB 16; Length 326;
Pred. No. 24;
2; Mismatches 0; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.8%; Score 49; DB 16; Length 99; Best Local Similarity 44.4%; Pred. No. 8.4; Matches 9; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C43733_1.pep
US-10-767-701-44199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
COTHER INFORMATION: Clone ID: LIB5048-010-R1-XP1-E2.pep US-10-767-701-51811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-146-473-76

Sequence 76, Application US/10146473

Publication No. US2003010888A1

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew

APPLICANT: Gout, Ivan

APPLICANT: Gte, Ali

APPLICANT: Gte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSDYKFYEDANGTRDHKK 18
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75 RTFYEYAVDSGGTEDHRK 92
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| ::||||||
162 SDYDEYYEDANGT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SDY-KFYEDANGT 13
                                                                                TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: UNSURE
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       SEQ ID NO 44199
LENGTH: 326
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                                                                                                                                                  FEATURE:
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Sequence 19, Application US/10359012

Sequence 19, Application US/10359012

Publication No. US20030232419A1

GENERAL INFORMATION:

APPLICANT: TERMAN, JOHN.

APPLICANT: TERMAN, JOHN.

APPLICANT: PASTERKAMP, Ronald J.

APPLICANT: PASTERKAMP, ROUGCULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT

TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT

TITLE OF INVENTION: AND METHODS OF USING THE SAME

FILE REPERBENCE: JHU1840-3

CURRENT APPLICATION NUMBER: US 60/384,302

PRIOR PILING DATE: 2002-05-30

PRIOR PELING DATE: 2002-05-30

PRIOR PILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: US 60/384,178

PRIOR APPLICATION NUMBER: US 60/354,178

PRIOR PILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: US 60/354,178

PRIOR APPLICATION NUMBER: US 60/354,178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
              APPLICANT: Catanutc, Paola
APPLICANT: Wiley, David J.
APPLICANT: Wiley, David J.
APPLICANT: You, Min
TITLE OF INVENTION: BOT1: Target for Antifungal Agents
FILE REFERENCE: 4052-24
CURRENT FILINO NUMBER: US/10/174,487
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US 60/298,901
PRIOR APPLICATION NUMBER: US 60/298,901
PRIOR SEQ ID NOS: 6
SOFTWARE: Patentin Version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
42.5%; Score 45.5; DB 1
Best Local Similarity 40.7%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Drosophila truncated mutant US-10-359-012-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 RSOYKFTNAKVGKVGYRYGSGNRDNKK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RSDYKF-----YEDANGTRDHKK 18
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US-10-425-114-68661
US-10-425-114-68661
Sequence 68661, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-174-487-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSDDESY--ANETREHKK 20
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APPLICANT: Verde, Fulvia
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 345
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Fublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REPRENCE: 38-21(5323.9)
CURRENT APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 152876
LENGTH: 75
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                                                                   FRIOR PELLICA NUMBER: 60/240,347

PRIOR FLILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-110-23

PRIOR FILING DATE: 2000-112-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-22

PRIOR PELLOGATION NUMBER: 60/267,636

PRIOR PELLOGATION NUMBER: 60/267,636

PRIOR PELLING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 3001-02-16

PRIOR FILING DATE: 301-02-16

SOFTWARE PRIOR APPLICATION NUMBER: 61/269,308

PRIOR FILING DATE: 301-02-16

SOFTWARE PRIOR APPLICATION 3.1

SEQ ID NO 72279

LENGTH: 1561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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US-10-424-599-152876
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Pred. No. 22;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.9%; Score 47; DB 15; Best Local Similarity 47.1%; Pred. No. 2.8e+02; Matches 8; Conservative 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (90) ... (90)
CTHER INFORMATION: X-any amino acid
US-10-282-122A-72279
                             FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/230,347
APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/10174487; Publication No. US20040106173A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKF-YEDANGTRDHKKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 DYKFYEDANGTRDHKKG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-10-174-487-4
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Sequence 287946, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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                                                                         Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION WHOBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 68661
LENGTH: 824
TYPF.
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Sequence 287968, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Cao, Vinua
APPLICANT: Cao, Vinua
APPLICANT: APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 287968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.1%; Score 45; DB 17; Length 867; Best Local Similarity 47.1%; Pred. No. 3.2e+02; Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: UC-ZMFLB73046D10_FLI.pep
US-10-425-114-68661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Clone ID: MRT4577_2571C.1.pep
US-10-425-115-287968
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 65128, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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113 DNKYHADKHGLQDAKKG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 DNKYHADKHGLQDAKKG 86
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAME/KEY: unsure
NAME/KEY: unsure
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Sequence 128610, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Noas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: La Noas J.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPL
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Stou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Caro, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 39-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 287946
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Diants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SRQ ID NO 65128
LENGTH: 972
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42.1%; Score 45; DB 17; Length 1118;
Best Local Similarity 47.1%; Pred. No. 4.1e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
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; OTHER INFORMATION: Clone ID: UC-ZMFLMO17067E07_FLI.pep
US-10-425-114-65128
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US-10-425-115-287946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.1%; Score 45; DB 15; Best Local Similarity 47.1%; Pred. No. 3.6e+02; Matches 8; Conservative 4; Mismatches 5
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APPLICANT: YU, Hung-Heiang
TITLE OF INVENTION: MULECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
TITLE OF INVENTION: AND METHODS OF USING THE SAME
FILE REPERENCE: JHU1840-3
CURRENT APPLICATION NUMBER: US/10/359,012
CURRENT FILING DATE: 2003-02-04
PRIOR FILING DATE: 2003-06-13
PRIOR FILING DATE: 2002-06-30
PRIOR PILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-04
PRIOR FILING DATE: 2002-05-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN NUMBER: US 60/354,178
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PATENTIN VERSION 3.1
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Sequence 20, Application US/10359012

Sequence 20, Application US/10359012

Sequence 20, Application No. US20030232419A1

GENERAL INFORMATION:

APPLICANT: TERMAN, Jon R.

APPLICANT: TERMAN, Jon R.

APPLICANT: MAC. Tianyi

FILE OF INVENTION: AND METHODS OF USING THE SAME

FILE REFERENCE: JHU1840-3

CURRENT APPLICATION NUMBER: US 60/388,325

PRIOR FILING DATE: 2002-06-13

PRIOR PLING DATE: 2002-06-13

PRIOR PLING DATE: 2002-06-04

PRIOR PLING DATE: 2002-06-04

PRIOR PLING DATE: 2002-02-04

NUMBER OF SEQ ID NOS: 40

SOFTWARE: Patentin version 3.1

SEQ ID NO 20

LENGTH: 3002

MAC. Tianyi

LENGTH: 3002

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SEQ ID NO 20

LENGTH: 3002

MAC. Tianyi

LENGTH: 3002

MAC. Tianyi

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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61.1%; Pred. No. 1.1e+03;
tive 2; Mismatches 3; Indels
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    PASTERKAMP, Ronald J.
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Matches 11; Conserv
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Sequence 12, Application No. US20030232419A1

GENERAL INFORMATION

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

APPLICANT: TERMAN, John R.

APPLICANT: TERMAN, John R.

APPLICANT: PASTERKAMP, Ronald J.

APPLICANT: WOLODKIN, Alex L.

APPLICANT: WAO, Tianyi

APPLICANT: WAD METHODS OF USING THE SAME

TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT

TITLE OF INVENTION: MOLECULES INTERACTING THE SAME

FILE REFERENCE: JHU1840-3

CURRENT APPLICATION NUMBER: US 60/388,325

FRIOR APPLICATION NUMBER: US 60/384,302

PRIOR PELING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: US 60/384,302

PRIOR APPLICATION NUMBER: US 60/384,302

PRIOR APPLICATION NUMBER: US 60/384,178

PRIOR APPLICATION NUMBER: US 60/384,178

PRIOR APPLICATION NUMBER: US 60/354,178

PRIOR APPLICATION NUMBER: US 60/354,178

PRIOR PLING DATE: 2002-02-04

NUMBER OF SEQ ID NOS: 40

SOFTWARE: PATENTING DATE: PATENTING DATE
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Pred. No. 1e+03;
2; Mismatches 3; Indels ;
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Publication No. US20030232419A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: KCLODKIN, Alex L.
APPLICANT: TERMAN, Jon R.
APPLICANT: MAO, Tianyi
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Pred. No. 4.6e+02;
0; Mismatches 5; Indels
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US-10-437-963-128610
                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KBY: unsure
LOCATION: (1)...(1245)
OTHER_INFORMATION: unsure at all Xaa locations
FILE REFERENCE: 38-21(51221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 128610
LENGTH: 1245
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 61.1%;
Matches 11; Conservative ;
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                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
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; ORGANISM: Drosophila
US-10-359-012-12
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LENGTH: 2734
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US-10-359-012-10
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APPLICANT: Wav, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Brabazuk, Brad

FILE APPLICANT: Brabazuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION UNBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

ESC ID NO 113950

LENGTH: 643
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 120244
LENGTH: 2932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
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US-10-437-963-120244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_1768C.1.pep
US-10-437-963-113950
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Pred. No. 1.6e+03;
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                                                                 Sequence 113950, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 120244, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 DFNFYEEKESARCAKKG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DYKFYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 YEROGGERDHNKG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 YEDANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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ORGANISM: Oryza sativa
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Sequence 8, Application US/10359012
| Publication No. US200302321991
| Publication No. US200302321991
| Publication No. US200302321991
| GENERAL INFORMATION:
| APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
| APPLICANT: TERMAN, JOH R.
| APPLICANT: TERMAN, TRAND, Ronald J.
| APPLICANT: PASTERRANP, Ronald J.
| APPLICANT: MAO, Tianyi
| APPLICANT: PASTERRANP, Ronald J.
| APPLICANT: PASTERRANP, RONALD S.
| TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT TITLE OF INVENTION: AND METHODS OF USING THE SAME
| TITLE OF INVENTION: AND METHODS OF USING THE SAME
| TITLE OF INVENTION: AND METHODS OF USING THE SAME
| TITLE OF INVENTION: WUMBER: US 60/384,302
| CURRENT FILING DATE: 2002-06-13
| PRIOR PILING DATE: 2002-06-13
| PRIOR PILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-510-424-599-170099
Sequence 170099, Application US/10424599
Sequence 170099, Application US/10424599
Sequence 170099, Application No. US/20040031072A1
GENERAL INFORMATION:
JAPPLICANT: La Rosa Thomas JAPPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 138-21 (51223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 170099
LENGTH: 399
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41.1%; Score 44; DB 15; Length 399;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 10; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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US-10-424-599-170099
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LOCATION: (1)..(399)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4526 RSDDESY--ANETREHKK 4541
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ORGANISM: Glycine max
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Best Local Similarity
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; ORGANISM: Drosophila
US-10-359-012-8
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               APPLICANT: DENOEL, PHILIPPE
APPLICANT: POOLMAN, JAN
APPLICANT: POOLMAN, JAN
APPLICANT: POOLMAN, JAN
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REFERENCE: B45210
CURRENT PAPLICATION NUMBER: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR PILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PASELSEQ FOR Windows Version 4.0
SEQ ID NO 3
LEWNTH: 13
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Bublication No. US20030096370A1

GENERAL INNORMATION:

APPLICANT: BERTHET, FRANCOIS-XAVIER

APPLICANT: DENOEL, PHILIPPE

APPLICANT: TOOLMAN, JAN

TITLE OF INVENTION: HARMOPHILUS INFLUENCA OUTER MEMBRANE

TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION

FILE REFERENCE: B45210

CURRENT FILING DATE: 2002-08-15

PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: PCT/EP01/01556

PRIOR APPLICATION NUMBER: GB 0003502.2

PRIOR FILING DATE: 2000-02-13

PRIOR FILING DATE: 2000-02-15

PRIOR FILING DATE: 2000-02-15
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: BERTHET, FRANCOIS-XAVIER APPLICANT: DENOEL, PHILIPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Haemophilus influenzae
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Best Local Similarity 77.0
-109 7; Conservative
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Matches 7; Conservative
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US-10-425-115-204064
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US-10-203-942-7
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Sequence 143107, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yshua

APPLICANT: Can, Yongwei

APPLICANT: Boukharco, Andrey A.

APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 143107

LEGTH: 1001

MANNER OF SED ID NOS: 204966
US-10-425-115-283230

Squence 283230, Application US/10425115
Squence 283230, Application US/10425115
Squence 283230, Application No. US2004021427241
Squence 283230, Application No. US2004021427241
Squence 283230, Towaration of the control of the
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40.7%; Score 43.5; DB 16; Length 1001;
Best Local Similarity 56.2%; Pred. No. 6.2e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.7%; Score 43.5; DB 17; Length 613; 50.0%; Pred. No. 3.8e+02; tive 3; Mismatches 5; Indels 1;
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US-10-437-963-143107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_21402C.1.pep

US-10-425-115-283230
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685 KLYEDSNGNFLGHRKG 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%
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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 160723
LENGTH: 274
                                                                                                                                                TYPE: PRT ORGANISM: Glycine max
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US-10-767-701-39724
                                                                                                                                                                                                                                 FEATURE:
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Publication No. US2004003107241
GENERAL INFORMATION:
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APPLICANT: La constant and the sequence of the sequence
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Sequence 50418, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

SEQ ID NOS: 63128

LENGTH: 154
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 204064
LENGTH: 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
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US-10-767-701-50418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: MRT4577_117695C.1.pep
US-10-425-115-204064
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 40.2%; Score 43; DB Best Local Similarity 47.4%; Pred. No. 77; Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 DYDFYXEEKANARRAEKRG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
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APPLICANT: LA ROSS, Thomas J.

APPLICANT: La Ross, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 10/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 128293

LENGTH: 1299
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; Sequence 39724, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Shou, Yihua
; APPLICANT: Cao, Yongwel
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associa;
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (53535) B
; CURRENT APPLICATION NUMBER: US/10/767,701
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 39724
; LENGTH: 337
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                                                                                 Query Match 40.2%; Score 43; DB 15; Length 274; Best Local Similarity 50.0%; Pred. No. 2e+02; Matches 8; Conservative 3; Mismatches 5; Indels
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US-10-767-701-39724
; OTHER INFORMATION: Clone ID: PAT_MRT3847_116150C.1.pep
US-10-424-599-160723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.2%; Score 43; DB 16;
53.3%; Pred. No. 2.5e+02;
tive 1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 128293, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                             4 YKFYEDANGTRDHKKG 19
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Best Local Similarity 53.23
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza Bativa
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31 SDYSF-SDANGDKGH 44

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Sequence 272502, Application US/10424599
Subblication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5)2123)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 272502
                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glater, Steven C.
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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US-10-424-599-272502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.7%; Score 42.5; DB 14; Best Local Similarity 42.1%; Pred. No. 8.8e+02; Matches 8; Conservative 5; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.3%; Score 42; DB 42.1%; Pred. No. 92; tive 5; Mismatches
                                                                                                      US-10-369-493-6568
. Sequence 6568, Application US/10369493
. Publication No. US20030233675A1
. GENERAL INFORMATION:
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'Sequence 135, Application US/10289762

'Publication No. US20040006218A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSDYKFYEDANGTRDHKKG 19
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Best Local Similarity 42.1
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Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: AND SON THOMAS J
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 285321
LENGTH: 202
                                                                                                                                                                                                                                                                                                                                        Sequence 162795, Application US/10424599
; Publication No. US20040031072A1
; Fublication No. US20040031072A1
; GENERAL INFORMATION:
; GENTERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
39.7%; Score 42.5; DB 15; Length 81;
Best Local Similarity 47.4%; Pred. No. 68;
Matches 9; Conservative 1; Mismatches 6; Indels
                                                                                  Length 1299;
                                                                            Query Match
40.2%; Score 43; DB 16; Length 12
Best Local Similarity 50.0%; Pred. No. 9.7e+02;
Matches 9; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_118021C.1.pep
; OTHER INFORMATION: Clone ID: PAT_MRT4530_30660C.1.pep
US-10-437-963-128293
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US-10-424-599-285321
                                                                                                                                                                                                               27 YMFRVDYADQTGRNEHKKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 YKF---YEDANGTRDHKKG 19
                                                                                                                                                                                2 SDYKFYEDANGTRDHKKG 19
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Best Local Similarity 60.07
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                         RESULT 35
US-10-424-599-162795
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US-10-424-599-285321
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NOS: 6849
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APPLICANT: Ku, H.
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
TITLE OF INVENTION Identification of Essential Genes in Microorganisms
TITLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/203
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 54860
LENGTH: 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.3%; Score 42; DB 15; Length 189; Best Local Similarity 50.0%; Pred. No. 1.9e+02; Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54860, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangeu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
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CRGANISM: Chlamydia pneumoniae
US-10-282-122A-54860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DYKFYEDANGTRDHKK 18
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50 DHKFDEETTINRDHFK 73
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0
Query Match
39.3%; Score 42; DB 15; Length 361;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 8; Conservative 2; Mismatches 6; Indels
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3 DYKFYEDANGTRDHKK 18

Search completed: November 24, 2004, 10:00:16 Job time: 72.663 Bec8

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                     November 24, 2004, 09:29:11; Search time 71.663 Seconds (without alignments) 94.040 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_EW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_EW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_EW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_EVBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US09_EWBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US106_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1575965 seqs, 354694765 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                        1 RSDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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98
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Match Length
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Maximum DB
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14 48 49 0 356 15 US-11-222-122A-6548 Sequence 6459, A 15 US-11-222-122A-6549 Sequence 6459, A 15 US-11-222-122A-6549 Sequence 6459, A 15 US-11-222-122A-6549 Sequence 6459, A 15 US-11-222-122A-6539 Sequence 15739, A 15 US-11-222-122A-6539 Sequence 15739, A 15 US-11-222-122A-6539 Sequence 15739, A 15 US-11-223-12273 Sequence 15739, A 15 US-11-223-12273 Sequence 15739, A 15 US-11-223-12273 Sequence 15739, A 15 US-11-223-12729 Sequence 15739, A 15 US-11-223-12729 Sequence 15739, A 15 US-11-223-12739 Sequence 15779, A 15 US-11-23-12739 Sequence 15779, A
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Sequence 4, Application US/10203942;
Sequence 4, Application US/10203942;
Sequence 4, Application US/10203942;
Publication No. US20030096370A1
GENERAL INFORMATION:
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: PROLMAN, JAN
APPLICANT: THONNARD, JOBELE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REFRENCE: B45210
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR PILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR APPLICATION NUMBER: 2000-02-15
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR APPLICATION NUMBER: PC7/EP01/0101/01556
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR APPLICATION NUMBER: PC7/EP01/01556
PRIOR APPLICATION NUMBER: PC7/EP01/0101/01556
PRIOR APPLICATION NUMBER: PC7/EP01/0101/01556
PRIOR APP
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RESULT 2

Sequence 4, Appli Sequence 21, Appli Sequence 37, Appli Sequence 9, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 142, Appli

US-10-203-942-4

US-10-203-942-8

US-10-36-940-37

US-10-36-840-37

US-10-33-942-9

US-10-203-942-6

US-10-203-942-6

US-10-203-942-6

US-10-613-765-2

US-10-613-765-2

US-10-613-765-2

US-10-613-765-142

19 353 353 353 311 22 311 8885 8885 9009

1000.0 1000.0 1000.0 88.8 833.2 803.2 500.0 500.0 500.0 500.0

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LENGTH: 353
TYPE: PRT
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Sequence 8, Application US/10203942

Publication No. US20030096370A1

FRENEAL INFORMATION:

APPLICANT: BERTHET, FRANCOIS-XAVIER

APPLICANT: DENOEL, PHILIPPE

APPLICANT: DOCHANN, JAN

TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE

TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE

TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE

TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION

FILE REFERENCE: B45210

CURRENT APPLICATION NUMBER: US/10/203,942

CURRENT FILING DATE: 2002-08-15

PRIOR PILING DATE: 2001-02-13

PRIOR PILING DATE: 2001-02-13

PRIOR PILING DATE: 2000-02-15

NUMBER OF SEQ ID NOS: 9

SOFTWARE PRESENCE FASTERE FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 98; DB 16; Length 353;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 98; DB 14; Length 28; Best Local Similarity 100.0%; Pred. No. 3.3e-08; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/10467421
Publication No. US20040116665A1
GENERAL INFORMATION:
APPLICANT: Berthet, Francois-Kavier Jacques
APPLICANT: Dencel, Philippe
APPLICANT: Dencel, Philippe
APPLICANT: Poolman, Jan
APPLICANT: Thomard, Jan
CURRENT PRING DATE: 2001-08-08
FRIOR PRING APPLICATION NUMBER: PCT/EP02/01361
PRIOR APPLICATION NUMBER: PCT/EP02/01361
PRIOR FILING DATE: 2002-02-08
PRIOR PILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
COCATION: (1)...(353)
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-467-421-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 RSDYKLYNKNSSTLKDLGE 150
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ORGANISM: Haemophilus influenzae
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LENGTH: 28
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Sequence 9, Application US/10203942

Publication No. US20030096370A1

GENERAL INFORMATION:

APPLICANT: BERTHET, FRANCOIS-KAVIER

APPLICANT: POOLWAN, JAN

APPLICANT: TOOLWAN, JAN

TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE

TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION

FILE REFERENCE: B45210

CURRENT APPLICATION NUMBER: US/10/203,942

CURRENT FILING DATE: 2002-08-15

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-02-15

PRIOR SPELICATION NUMBER: GB 0003502.2

PRIOR SPELICATION NUMBER: GB 0003502.2

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PRECSEQ for Windows Version 4.0

SES ID NO 9

SES ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 87; DB 14; Length 352;
Pred. No. 3e-05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87; DB 14; Length 353; Pred. No. 3e-05;
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Sequence 37, Application US/10336840
Publication No. US20030219454A1
GENERAL INFORMATION:
APPLICANT: TERRY, TAMSIN DEBORAH
APPLICANT: TSENG, HSING-JU
APPLICANT: HOBB, RHONDA IVY
APPLICANT: HOBB, RHONDA IVY
APPLICANT: DENNINGS, MICHAEL PAUL
APPLICANT: DOWNES, JOHN
TITLE OF INVENTION: HARMAGGLUTININ ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                             FILE REPERENCE: 37955-0007
CURRENT APPLICATION NUMBER: US/10/336,840
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/AU01/00822
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
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'Sequence 2, Application US/10203942

'Publication No. US20030096370Al

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 RSDYKLYNENSSTLKKLGE 150
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; TYPE: BRT
: ORGANISM: Haemophilus influenzae
US-10-336-840-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RSDYKLYNKNSSTLKDLGE 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.8%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Gaps
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                                                                 APPLICANT: Mindrinos, Michael N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: BF82 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
FILE REFERENCE: 00786/254002
CURRENT APPLICATION NUMBER: 2001-05-29
CURRENT PILING DATE: EARLIER PILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/310,912
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1994-09-22
PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
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APPLICANT: Staskawicz, Brian J.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Breent, Andrew F.
APPLICANT: Banlbeck, Douglas
APPLICANT: Katagiri, Fumiaki
APPLICANT: Katagiri, Fumiaki
APPLICANT: Winkel, Barbara N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
ITILE OF INVENTION: RESC GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: BETECTION METHODS
FILE REFERENCE: 00786/254004
CURRENT PILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 09/867,852
PRIOR APPLICATION NUMBER: US 09/801,085
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1994-04-13
PRIOR FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 214
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 885; 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10613472
Publication No. US20040088756A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 ADYKLCKKVSAILKSIGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SDYKLYNKNSSTLKDLGE 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana US-09-867-852-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Arabidopsis thaliana US-10-613-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                      unkel, Barbara N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 885
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                                      APPLICANT: POCKMAN, JAN.
APPLICANT: THONNARD, JOELLE
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REFERENCE: B45210
CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR FILING DATE: 2000-02-13
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DEDORGE, PHILIPPE
TITLE OF INVENTION: HERMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: HERMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REFERENCE: B45210
CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP01/01556
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR PILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 6
LENTH: 31
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Llarity 81.8%; Pred. No. 1.4e-05;
Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; DB 14;
9.9e-06;
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FRANCOIS-XAVIER PHILIPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-203-942-6; Sequence 6, Application US/10203942; Publication No. US20030096370A1
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Patent No. US20020147324A1
GENERAL INFORMATION:
APPLICANT: Augubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Haemophilus influenzae
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Best Local Similarity
Matches 18; Conserva
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Best Local Similarity
Matches 18; Conserv
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APPLICANT: NUMBER: SALVATA STATES STA
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                                                                                                                                                                                                           9; Length 909;
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TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
                                                                                                                                                                                             DB /
                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                               Score 49;
Pred. No.
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Publication No. US20040172673A1
GENERAL INFORMATION:
APPLICANT: ATAGIRI, FREDERICK M.
APPLICANT: STASKAWICZ, BRIAN J.
APPLICANT: KATAGIRI, PUMIAKI
APPLICANT: MINDRINOS, MICHAEL N.
APPLICANT: MINDRINOS, MICHAEL N.
APPLICANT: UGO-LIANG
APPLICANT: ELLIS, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 142, Application US/10613472
Publication No. US20040088756Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ausubel, Frederick M. APPLICANT: Staskawicz, Brian J. APPLICANT: Brent, Andrew F. APPLICANT: Dablbeck, Douglass APPLICANT: Katagiri, Fumiaki APPLICANT: Kunkel, Barbara N.
                                                                                                                                                                                                                                                                                                                                                                                                            111 ADYKLCKKVSAILKSIGE 128
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111 ADYKLCKKVSAILKSIGE 128
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                                                                  TYPE: PRT CRGANISM: Arabidopsis thaliana US-09-867-852-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                        Query Match 50.0%;
Best Local Similarity 55.6%;
Matches 10; Conservative
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Best Local Similarity 55.65
Matches 10; Conservative
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   SEQ ID NO 142
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Sequence 142, Application US/09867852

GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Stackawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Kunkel, Barbara N.
APPLICANT: Kunkel, Barbara N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Wolcilang Michael N.
APPLICANT: WONGER: BREATHER APPLICATION NUMBER: 09/301,085
PRIOR PLILING DATE: EARLIER FILING DATE: 1999-04-28
PRIOR PLILING DATE: EARLIER FILING DATE: 1994-08-22
PRIOR PLILING DATE: EARLIER PILING DATE: 1994-04-13
NUMBER OF SEO ID NOS: 200 D.
NUMBER OF SEO ID NOS: 200 D.
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APPLICANT: STASKAMICZ, BRIAN J.
APPLICANT: KATAGIRI, FUMIAKI
APPLICANT: KATAGIRI, FUMIAKI
APPLICANT: MINDRINOS, MICHAEL N.
APPLICANT: YU, GUO.LIANG
APPLICANT: BARBARA
APPLICANT: BARBARA
APPLICANT: BARBARA
APPLICANT: BARBARA
APPLICANT: SALMERO, JOHN
TITLE OF INVENTION: DETECTION METHODS
TITLE OF INVENTION: DETECTION METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
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Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 00786/254005
CURRENT APPLICATION NUMBER: US/10/613,765
CURRENT FILING DATE: 2003-07-02
PRIOR PELICATION NUMBER: US 09/867,852
PRIOR PELING DATE: 2001-05-29
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1999-04-28
PRIOR PELING DATE: 1994-09-22
PRIOR PELING DATE: 1994-09-22
PRIOR PELING DATE: 1994-09-13
NUMBER OF SEQ ID NOS: 214
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 208
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                      Sequence 2, Application US/10613765 Publication No. US20040172673A1 GENERAL INFORMATION:
103 ADYKLCKKVSAILKSIGE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 ADYKLCKKVSAILKSIGE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-765-2
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                            US-10-613-765-2
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us-09-719-379a-4.rapb

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Sequence 45804, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; LOCATION: (175)...(175)
; OTHER INFORMATION: X=any amino acid
US-10-282-122A-45498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                       TYPE: PRT
ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||
14 YKLYNKPFDKLKDL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 YKLYNKNSSTLKDL 17
                                                                                                                                                           NAME/KEY: MISC FEATURE LOCATION: (93)...(93)
OTHER INFORMATION: X=any
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APPLICANT: Xu, H.

APPLICANT: Xu, H.

ILLE REPERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 00/2020

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-35

PRIOR PILING DATE: 2000-05-36

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/250,308

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06
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SOFTWARE: PatentIn version 3.1
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Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
TITLE OF INVENTION: DETECTION METHODS
PILE REFERENCE: 00786/254005
CURRENT APPLICATION NUMBER: US/10/613,765
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 09/867,852
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 1999-04-28
PRIOR PILING DATE: 1994-09-22
PRIOR APPLICATION NUMBER: US 08/310,912
PRIOR APPLICATION NUMBER: US 08/310,912
PRIOR APPLICATION NUMBER: US 08/27,360
PRIOR APPLICATION NUMBER: US 08/27,360
PRIOR PILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 214
SOFTWARE: PSECSE for Windows Version 4.0
SEQ ID NO 142
LENGTH: 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45498, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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111 ADYKLCKKVSAILKSIGE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-765-142
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
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APPLICANT: Wall, Daniel
APPLICANT: Graft
APPLICANT: Graft
APPLICANT: Graft
APPLICANT: Graft
APPLICANT: Cart Graft
APPLICANT: AND APPLICANT: Name of Selection of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
FILE REFERENCE: ELITRA.034
CURRENT FILING DATE: 2000-03-21
FILE REPLICATION NUMBER: 60/191,078
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR PILING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-26
FRIOR PELING DATE: 2000-05-26
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-110-23
FRIOR PELING DATE: 2000-12-2-16
FRIOR PELING DATE: 2001-12-2-16
FRIOR FILING DATE: 2001-12-3-16
FRIOR FRIOR
                                                                                                                        Gaps
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Score 48; DB 15; Length 365;
Pred. No. 41;
0; Mismatches 4; Indels
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Sequence 167399, Application US/10437963
; Sequence 167394, Application US/10437963
; Publication No. US20040123343A1
; BAPLICANT: La Rosa, Thomas J.
APPLICANT: Eas Rosa, Thomas J.
APPLICANT: Ca. Yongwei
; APPLICANT: Ca. Yongwei
; APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 19132218
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-65-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 167399
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 52221
LENGTH: 648
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46.9%; Score 46; DB 16; Length 1197;

Best Local Similarity 50.0%; Pred. No. 3.2e+02;

Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.9%; Score 46; DB 15; Length 648; Best Local Similarity 47.4%; Pred. No. 1.6e+02; Matches 9; Conservative 3; Mismatches 7; Indels
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US-10-437-963-167399
                         FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                        CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-12-20
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-282-122A-52321
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Sequence 9, Application US/10008355

Publication No. US20020164759A1

Sequence 9, Application US/10008355

Publication No. US20020164759A1

APPLICANT: Travis, James

APPLICANT: Decempa, Jan San APPLICANT: Banbula, Agnieszka

TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use

TITLE OF INVENTION: Dipeptidylpeptidases And Methods Of Use

CURRENT FILING DATE: 235.00440101

CURRENT FILING DATE: 2001-11-08

PRIOR PEDLICATION NUMBER: US 60/246,827

PRIOR PELLING DATE: 2000-11-08

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.0

SEQ ID NO 9

LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 536;
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Pred. No. 1.3e+02;
3; Mismatches 3; Indels
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Pred. No. 63;
0; Mismatches
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                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (420)...(420)
COTHER INFORMATION: X=any amino acid
US-10-282-122A-45804
  LOCATION: (369)..(369)
OTHER INFORMATION: X=any amino acid
                                                                                 NAME/KEY: MISC FEATURE
LOCATION: (371)...(371)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                        NAME/KEY: MISC FEATURE
LOCATION: (406)...(406)
OTHER INFORMATION: X=any amino acid
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; ORGANISM: Porphyromonas gingivalis
US-10-008-355-9
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APPLICANT: Zamudio, Carlos
APPLICANT: Amone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4%;
Matches 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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47 EYDLYNPNGTSLKD 60
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1 RSDYKLYNKNSSTLKDLG 18
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187 RDDYKVYNIEESHMED 202
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(7
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US-10-032-585-7797
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Squence 13, Application US/10435766

Relication No. US20030228616A1

GENERAL INCPRARTION:

APPLICANT: Strategene
APPLICANT: Sorge, Joseph A
APPLICANT: Hansen, Connie J
TITLE OF INVENTION:

TOTALE OF INVENTION:

APPLICANT: Hansen, Connie J
TITLE OF INVENTION:

APPLICANT: Hansen, Connie J
TITLE OF INVENTION:

APPLICANT: Hansen, Connie J
TITLE OF INVENTION:

PLE REFERENCE: 25436/1565C
CURRENT APPLICATION NUMBER: US/10/435,766
CURRENT FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2001-06-29
PRIOR PELING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/162,600
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 1000-10-27
PRIOR APPLICATION NUMBER: PCT/US00/29706
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 1099-10-29
PRIOR PILING DATE: 2000-10-27
PRIOR PELING DATE: 2000-10-27
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; Publication No. US20030180953A1
; Fublication No. US20030180953A1
; Fublication No. US20030180953A1
; GENERAL INFORMATION:
A APPLICANT: Charles, Boone
; APPLICANT: Charles, Boone
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bush
; TITLE OF INVENTYON: Gene Disruption Methodologies for Drug Target Discovery
; TILLE REPREBENCE: 10182-005-999
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7797
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LOCATION: (1118)..(1118)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature; LOCATION: (1123); LOCATION: (1123); OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-10-435-766-13
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61.5%; Pred. No. 5.2e+02;
tive 3; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Thermococcus strain TY
                                    | |||:||
724 RDDYKIYNIEESHMED 739
   1 RSDYKLYNKNSSTLKD 16
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1161 KLYNENPNVLKDM 1173
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Best Local Similarity 61.5*
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US-10-032-585-7797
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LENGTH: 1829
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Sequence 13272. Application US/10437963

Sequence 13272. Application US/10437963

Sequence 13272. Application No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Application No. William No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Exvalic, David K.
APPLICANT: Exvalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132673
LENGTH: 850
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Query Match 45.9%; Score 45; DB 14; Length 624; Best Local Similarity 50.0%; Pred. No. 2.2e+02; Matches 9; Conservative 2; Mismatches 7; Indels
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US-10-437-963-132722
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45.9%; Score 45; DB 16; L
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 3; Mismatches 5;
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OTHER INFORMATION: unsure at all Xaa locations
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Sequence 167391, Application US/10437963

Sequence 167391, Application US/10437963

Sequence 167391, Application No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Rovalic, David K.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Fing

APPLICANT: Butharuk, Brad

APPLICANT: Butharuk, Brad

APPLICANT: Butharuk, Brad

APPLICANT: Butharuk, Brad

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andr
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.9%; Score 45; DB 16; Length 1148; Best Local Similarity 50.0%; Pred. No. 4.4e+02; Matches 8; Conservative 3; Mismatches 5; Indels C
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_34607C.1.pep
US-10-437-963-132660
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SEQ ID NO 132660
LENGTH: 1148
TYPE: TYPE: TYPE: TYPE: TYPE: NAME/KEY: unsure
NAME/KEY: unsure
LOCATION: (1)..(1148)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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749 RDDYKVYNIEESHMED 764
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Matches 8; Conservative
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ORGANISM: Oryza sativa
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APPLICANT:
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APPLICANT:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Kovalic, David K.
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 -21(53.21)B
CURRENT APPLICANTON NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132719
LENGTH: 1127
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION VUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                   Length 850;
                                                                                                                                                                                                                                                                                                Query Match 45.9%; Score 45; DB 16; Length 85
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 8; Conservative 3; Mismatches 5; Indels
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US-10-437-963-132673
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US-10-437-963-132719
                                     FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(850)
FEATURE INFORMATION: unsure at all Xaa locations
FEATURE:
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; Sequence 132719, Application US/10437963
; Publication No. US20040123343A1
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Publication No. US20040123343A1
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |||:|| | ::|
595 RDDYKVYNIEESHMED 610
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591 RDDYKVYNIEESHMED 606
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Matches 8, Conservative
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             ORGANISM: Oryza sativa
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TILLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT PRILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132773
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Publication No. US20040123343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: W., Wel
APPLICANT: W., Wel
APPLICANT: W., Wel
APPLICANT: W., Wel
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 8; Conservative 3; Mismatches 5; Indels (
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                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_34720C.1.pep
US-10-437-963-132786
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US-10-437-963-132773
                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(1340)
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 132773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
CURRENT FILING DATE: 2003-05-14 WINDERN OF SEQ ID NOS: 204966 SEQ ID NO 132786 LENGTH: 1340
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                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
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US-10-437-963-132723
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Exourtic David K.
APPLICANT: Exourtic David K.
APPLICANT: Exourtic David K.
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bribazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REPERRNCE: 38-21(5)221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132777
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Sequence 132786, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
PAPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE FERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
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US-10-437-963-132735
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US-10-437-963-132777
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 112735
LENGTH: 1310
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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799 RDDYKVYNIEESHMED 814
                                                                                                                                                                                                                                                                                                                                                                                                        1 RSDYKLYNKNSSTLKD 16
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                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
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US-10-437-963-132786
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US-10-437-963-132777
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Sequence 132820, Application US/10437963

Sequence 132820, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: A Road, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Bucharow, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Bindey A.
APPLICANT: Bindey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barbaruk, Brad
APPLICANT: Barbaruk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/66
SEQ ID NOS: 204966
LENGTH: 1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%; Score 45; DB 16; Length 1479; 50.0%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34661C.1.pep
US-10-437-963-132720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT4530_34756C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132720
LENGTH: 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 132825, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
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871 RDDYKVYNIEESHMED 886
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Best Local Similarity 50.0%
Matches 8; Conservative
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Best Local Similarity 50.0%
--hos 8; Conservative
                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
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Sequence 132727, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Cao, Vinua
APPLICANT: Cao, Vinua
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATON NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 132727

LENGTH: 1391
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
LENGTH: 1386
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45.9%; Score 45; DB 16; Length 1386;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 8; Conservative 3; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%; Score 45; DB 16; Length 1391; 50.0%; Pred. No. 5.4e+02; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_34664C.1.pep
US-10-437-963-132723
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US-10-437-963-132727
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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855 RDDYKVYNIEESHMED 870
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                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
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US-10-437-963-132720
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US-10-437-963-132727
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DEPLICANT: LAW AND AND AND AND AND APPLICANT: LAW AND APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Shou, Yihua APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Wei APPLICANT: Wei APPLICANT: Wei Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 199679
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50.0%; Pred. No. 7.2e+02;
tive 3; Mismatches 4; Indels (
                                                                                 Score 44; DB 14; Length 1216;
Pred. No. 6.7e+02;
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US-10-437-963-199679
                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                              Sequence 199679, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
      ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1505
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1114 RDDYKIYDQNEKNL 1127
                                                                                 44.9%;
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284 RMYNRYSSILKNLG 297
                                                                                                                                                            5 KLYNKNSSTLKDLG 18
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                                                            Query Match
Best Local Similarity 57.2.
Best Local 8; Conservative
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Matches 7; Conservative
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ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryza sativa
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US-10-437-963-199679
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US-10-437-963-112611
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US-10-369-493-1505

Sequence 1505, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Goa, Yongweist

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Winther Steven C.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: USABLE: US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

FRIOR FILING DATE: 2002-02-21

PRIOR FILING DATE: 2002-02-21

PRIOR FILING DATE: 2002-02-21

SEQ ID NO 1505

LENGTH: 1216
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Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Steven C.

APPLICANT: Gldman, Barry S.

TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERIES

FILE REFERENCE: 38-10(52052)B

CURRENT PILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR SEQ ID NOS: 47374

SEQ ID NO 22153
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45.9%; Score 45; DB 16; Length 1693;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.9%; Score 44; DB 14; Length 1058; 60.0%; Pred. No. 5.8e+02; tive 0; Mismatches 6; Indels
                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT4530_34751C.1.pep
US-10-437-963-132820
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132820
LENGTH: 1693
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; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22153
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833 RDDYKVYNIEESHMED 848
                                                                                                                                                                                                                                                                                                  1 RSDYKLYNKNSSTLKD 16
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Matches 9; Conservative
                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
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US-10-369-493-22153
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## Seq
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Sequence 195626, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Town Yilua
APPLICANT: Cav Yongwei
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILLE REPERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 195626

LENGTH: 87
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                                                                                                                         Length 1539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.9%; Score 43; DB 15; Length 88; 53.3%; Pred. No. 51;
                                                                                                                 Query Match 44.9%; Score 44; DB 16; Length 15
Best Local Similarity 37.5%; Pred. No. 8.8e+02;
Matches 6; Conservative 6; Mismatches 4; Indels
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US-10-424-599-276118
; OTHER INFORMATION: Clone ID: PAT_MRT4530_1647C.1.pep
US-10-437-963-112611
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OTHER INFORMATION: ungure at all Xaa locations
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922 YRVYNKNKGTVEETAD 937
                                                                                                                                                                                                                                                                                     4 YKLYNKNSSTLKDLGE 19
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54 SNHNLYNKNSPQLR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
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Matches 8; Conserve
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Best Local Similarity
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US-10-424-599-195626
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        3 DYKLYNKNSSTLKDL
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Search completed: November 24, 2004, 10:00:15 Job time : 72.663 Bec8

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Best Local Similarity 100.0%; Pred. No. 1.2e-08;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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AAH67570
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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RA Gousset N., Rosenau A., Sizaret P.Y., Quentin R.;

"Nucleotide sequences of genes coding for fimbrial proteins in a ryptic genospecies of Haemophilus spp. isolated from neonatal and genital tract infections.";

"Infect. Immun. 67:8-15(1999).

"Infect. Immun. 67:8-15(1999).

"Infect. Immun. 67:8-15(1999).

"C SIMILARITY: Belongs to the ompA family.

REMBI, AJ007317; CA407454.1; -..

REMBI, AJ007317; Couter membrane; IEA.

GO; GO:0005279; C:outer membrane (sensu Gram-negative Bacteria); IEA.

RO; GO:0005199; F:structural molecule activity; IEA.

RO; GO:0005199; F:structural molecule activity; IEA.

InterPro; IPR006665; OmpA/MoctB.

InterPro; IPR006665; OmpA/MoctB.

InterPro; IPR006665; OmpA/mem.

RIMERPRO; IPR00699; OmpA_timem.

Refam; PP00691; OmpA, IERE.

REMBI, PR01899; OmpA_timem.

Refam; PP01899; OmpA_timem.

Refam; PP01899; OmpA_timem.

Refam; PP01899; OmpA_timem.
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Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Coeanobacillus iheyensis isolated from the Iheya
Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
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85.7%; Pred. No. 1.6;
tive 0; Mismatches 1; Indels 1
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                                  086254;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Outer membrane protein (Fragment).
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Last annotation update)
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       360 AA
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EMBL; AP004594; BAC12475.1; -.
InterPro; IPR010462; Ectoine synth.
InterPro; IPR011051; RmLC like cupin.
Pfam; PF06339; Ectoine_synth; I.
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99081716; PubMed=9864189;
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PRINTS; PRO1022; OUTRAMBRANEA.
PRODOM; PD000930; OMPA/MOCB; 1.
PROSITE; PS01068; OMPA; 1.
NON TER 360 A8; 38415 MW; A3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 RSDYKFY-DANGAR 152
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OrderedLocusNames=OB0519;
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nes 12; Conservative
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                                                                                                                                                                                                                                                                    Haemophilus sp.
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Matches
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MEDLINE-9422575; PubMed=7909539;
SITRAIN-WTHI 1128;
STRAIN-WTHI 1128;
SITRAIN-WTHI 1128;
SITRAIN-WTHI 1128;
Demaria T., Rolattukudy P.B., Murwin D., Billy J., Leake E., Lim D., Demaria T., Bakaletz L.;
Paralle T., Bakaletz L.;
"Role of fimbriae expressed by nontypeable Haemophilus influenzae in pathogenesis of and protection against otitis media and relatedness of the fimbrin subunit to outer membrane protein A.";
Infect. Immun. 62:2002-2020(1994).
--- FUNCTION: Acts as a fimbriae subunit.
--- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
--- SIMILARITY: Belongs to the ompA family.
       Gaps
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Pasteurellaceae; Haemophilus.
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       0; Indels
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By similarity.

OmpA-like.

576B1C59B4818C37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Outer membrane protein P5 precursor (OMP P5) (Fimbrin)
Name-omph, Synonyms-ompP5;
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                      359 AA
   0; Mismatches
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InterPro; IPR006664; Bac OmpA.
InterPro; IPR002368; OmpA.
InterPro; IPR006665; OmpA/MoctB.
InterPro; IPR006690; OMPA_LIKE.
InterPro; IPR00498; OmpA_LIKE.
                                                                                                                   1 RSDYKFYEDANGTRDHKKG 19
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278 322 O
359 AA; 38340 MW;
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Best Local Similarity 100.
Matches 19; Conservative
       19; Conservative
                                                                                                                                                                                                                                                                                                                                          STANDARD;
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359
344
322
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P45996;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Robert S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevichenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalsku U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M.,
Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotherical protein FLJ20760 (Hypothetical protein FLJ20729)
Name=FLJ20729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO00767; BAA91371.1; -.
EMBL; BC026236; AAH26236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 470 Aa; 53918 MW; 34ASOAlC62E4F4E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                      470 AA
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                                                                                                        PRT;
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SDYRFLEDVARTADH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDYRFLEDVARTADH 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SDYKFYEDANGTRDH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
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                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                            Homo sapiens (Human)
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es 9; Conserv
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                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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01-OCT-2002
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208
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Q9H3X3;
                                                                                                                             O9NWK9;
                                                                                                        Q9NWK9
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                                                             RESULT 7
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ID Q9
AC Q9
DT 01
DT 01
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawakani T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to EMEL/GenBank/DDBJ databases.

EMBL, AKO00736; BAA91349.1.

SEQUENCE 294 AA, 34673 MW; 286F47253B9435ED CRC64;
                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR.2001 (TrEMBLrel. 16, Created)
01-MAR.2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Serologically defined breast cancer antigen NY-BR-75 (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Breast;

MEDLINE=22633220; PubMed=12747765;

Scanlan M.J. Gout I., Gordon C.M., Williamson B., Stockert E.,

Gure A.O., Jager D., Chen Y.T., Mackay A., O'Hare M.J., Old L.J.;

Gure A.O., Jager D., Chunan breast cancer: antigen definition and

quantitative analysis of mRNA expression.";

Cancer Immun. 1:4-4(2021).

EMBL; AR308296; AAG48263.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%; Score 49; DB 2; Length 305; 60.0%; Pred. No. 21; ive 1; Mismatches 5; Indels
                                                           Query Match 45.8%; Score 49; DB 2; Length 128; Best Local Similarity 60.0%; Pred. No. 8.2; Matches 9; Conservative 1; Mismatches 5; Indels
Complete proteome.
SEQUENCE 128 AA; 14763 MW; 17F4909F5AD64D6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 AA; 35783 MW; 48B3112D59F88520 CRC64;
                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ20729.
                                                                                                                                                                                                                                                                                                       294 AA
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                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                 S KPYEDANGTRDHKKG 19
                                                                                                                                                                          | || || || || || || KSLEDIQGTEDHQKG 18
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Best Local Similarity 60.0.
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nes 9; Conservative
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Matches

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RESULT 6
091278
1D 091278
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1D 01-M
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A PubMed=15077118; DOI=10.1038/nbt959;
A Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Heidelberg J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
A Colonay J.F., Eisen J.A., Fouts D.E., Haft D.H., Selengut J.,
A Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
A Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
A Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Feldblyum T.V., wall J.D., Voordouw G., Fraser C.M.;
The genome sequence of the anaerobic, sulfate-reducing bacterium
I Desulfovibrio vulgaris Hildenborough.";
I Nat. Biotechnol. 22:554-559(2004).
R EMBL, AEG17314; AASS60811; -.
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Desulfovibrionaceae; Desulfovibrio.
NCBL_TaxID=882;
                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                         Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL442074; CAC09440.1; -.
                                                                                                                                                                                                                                                              470 AA; 53846 MW; 9E87A1A99C05C9E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 AA; 59893 MW; C6D54A537BBCC286 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Metallo-beta-lactamase family protein.
OrderedLocusNames=DVUI530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%; Score 49; 56.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR001279; Blactmase-like.
Interpro; IPR011108; RWMBL.
Pftan; PP00753; Lactamase_B; 1.
Pfam; PF07521; RWMBL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS96008 PRELIMINARY; PRT;
AAS96008;
27-APR-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                             2 SDYKFYEDANGTRDH 16
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Best Local Similarity 56.27
Conservative 9; Conservative
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nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                            Hypothetical protein.
                        Homo sapiens (Human)
  Name=DKFZp434M1929;
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
                                                                                     NCBI_TaxID=9606;
                                                                                                                                                    TISSUE-Testis;
                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q72BV4;
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                                                                                                                                                                                                                                                                                                                                                    Matches
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Q728V4

Q728V4

Q728V4

Q728V4

DT 05-JU

DT 0
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ID AAS9
AC AAS9
DT 27-A
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STRAIN=0157:H7 / RIMD 0509952 / EHEC;
MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
Hayashi T., Makino K., Ohnishi W. Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shina T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli Complete genome comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                      Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordoww G., Praser C.M.; The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough."; sulfate-reducing bacterium EMEI, AE017314, A&S9608.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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-!- SUBUNIT: Homotrimer (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                       Bacteria, Proteobacteria, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio.
                                                                                                                                         Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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-!- SIMILARITY: Belongs to the Gram-negative porin family.
EMBL, AP002557; BAB35499.1, -.
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:006741; C:integral to membrane; IEA.
GO, GO:005741; C:intechnodrial outer membrane; IEA.
InterPro; IPR003229; OMP.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 AA; 59893 MW; C6D54A537BBCC286 CRC64;
27-APR-2004 (TrEMBLrel. 27, Last sequence update) 11-MAY-2004 (TrEMBLrel. 27, Last annotation update) Metallo-beta-lactamase family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Putaive outer membrane porin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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InterPro; IPR001702; Porin_Gram-ve.
Pfam, PF00267; Porin_1; 1.
PRINTS; PR00183; ECCLNEIPORIN.
PRINTS; PR00182; ECCLNEIPORIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 ADYLFLESTYGDRDHK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SDYKFYEDANGTRDHK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=ECs2076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 56.2.
Best Local Similarity 50.2.
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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PRT;
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Matches 10; Conservative
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                                PRELIMINARY;
                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.;
                                                                                                                                                                                                                                                                                                Wilson R.;
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Q9GYL4
Q9GYL4
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                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 408:529-533 (2001).
-1- SUBUNIT: Homotrimer (By similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete protecme; Membrane; Outer membrane; Porin; Transmembrane. SEQUENCE 366 AA; 41025 MW; 9B16735B9BBA9F25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Bscherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074933; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                        ï
                                                                                                44.4%; Score 47.5; DB 2; Length 366; 62.5%; Pred. No. 44; 1ve 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.4%; Score 47.5; DB 2; Length 366; 62.5%; Pred. No. 44; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (By similarity).

-!- SIMILARITY: Belongs to the Gram-negative porin family.
EMBL; AR005358; AAG56297.1; -.
PIR, D9088; D9088.
PIR, B85729; E85729.
HSSP; P02931; 1GFN.
            ProDom, PD000808; OMP 2; 1.
PROSITE; P800576; GRAM, NGG PORIN; 1.
Membrane; Outer membrane; Porin; Transmembrane.
SEQUENCE 366 AA; 41025 MW; 9816735B9BBA9F25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P02931; IGFN.
GO; GO: 0016021; C: integral to membrane; IEA.
GO; GO: 0015281; C: integral to membrane; IEA.
GO; GO: 0015288; F: porin activity; IEA.
GO; GO: 0005215; F: transporter activity; IEA.
GO; GO: 0006210; F: transport; IEA.
InterPro; IPR001229; OMP 2.
InterPro; IPR001897; Porin bac.
InterPro; IPR001802; Porin Gram-ve.
                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Putative outer membrane porin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00267; Porin_1; 1.
PRINTS; PR00183; ECOLIPORIN.
PRINTS; PR00182; ECOLNEIPORIN.
ProDom; PD000808; OWP 2; 1.
PROSITE; PS00576; GRAM_NEG_PORIN; 1.
                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                       3 DYKFYED-ANGTRDHK 17
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80 DFKGYNDEANGSRDNK 95
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DFKGYNDEANGSRDNK 95
                                                                                                                  Local Similarity 62.5
ses 10; Conservative
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ses 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=z2239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                               01-MAR-2002
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                                                                                                     Query Match
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Matches
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RESULT 13

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Gaps
                                                                                                                                                                               Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altefi H., Nguyen M., Lam B., Southwick A., Maranda M., Brooks S.,
Buehler B., Chao Q., Chin C., Chiou J., Choi B., Gonzalez A.,
Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ë,
                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 997;
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; R04E5-8; CE04800.
Hypothetical protein.
SEQUENCE 997 AA; 111954 MW; F1620378EF0D9DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothet.toal protein R04E5.8.
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997 AA.
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                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; Pubmed-9851916;
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SDEKLYKGIHGYTDHKAG 168
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                                                                                         Q8L789;
                                                                            Q8L789
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Matches
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Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                            A GOS GO: 0000151; Cubiquitin ligase complex; IEA.

R GO; GO: 0000151; F: nucleic acid binding; IEA.

GO; GO: 0000842; F: nucleic acid binding; IEA.

GO; GO: 00008270; F: nucleic acid binding; IEA.

R GO; GO: 0008270; F: nucleic non binding; IEA.

R GO; GO: 0016567; P: protein ubiquitination; IEA.

R InterPro; IPR00141; Zif CCCH.

R Pfam; PF00097; Zf-CCH; 1.

R SMART; SM00184; RING; 1.

R SMART; SM00184; RING; 1.

R SMART; SM00356; ZnF C3H1; 1.

R PROSITE; PS50089; ZF RING; 1.

R PROSITE; PS50089; ZF RING; 1.

M Metal-binding; Zinc; Zinc-finger.

O SEQUENCE 304 AA; 34215 MW; 7C107FA164251D27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK118376; BAC42988.1; -

EMBL; AK118376; BAC42988.1; -

RSPEP; PISP19; IRMD.

GO; GO:0000151; Cubiquitin ligase complex; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0016567; P:protein ubiquitination; IEA.

InterPro; IPR001651; Znf_CCCH.

InterPro; IPR01841; Znf_Ting.

Fram; PF00097; Zf_C34C4;

Pfam; PF00097; Zf_C34C4;

Pfam; PF000642; Zf_C34C4;
                                                                                                                                                                                                                                                         Score 47; DB 2; Length 304;
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.9%; Score 47; DB 2; Length 343; 50.0%; Pred. No. 50; ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00356; ZRF C3H1; 1.

PROSITE; PS00518; ZF RING 1; UNKNOWN 1.

PROSITE; PS50089; ZF RING 2; 1.

Hypothetical protein; Metal-binding; Zinc; Zinc-finger.

SEQUENCE 343 AA; 38719 WW; E333D70369C31A83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein At1g01350/F6F3_27.
Name=At1g01350/F6F3_27;
Arabidopsis thaliana (Mouse-ear cress).
-!- SIMILARITY: Contains 1 RING-type zinc finger.
EMBL; AC023628; AAF97335.1; -.
PIR; G86143; G86143.
                                                                                                                                                                                                                                                                                                                                                                                                 343 AA
                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                          || || |: :| ||| ||
151 SDEKLYKGIHGYTDHKAG 168
                                                                                                                                                                                                                                                                                                          2 SDYKFYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                      43.9%;
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Best Local Similarity 50.00,
Best and 9; Conservative
                                                                                                                                                                                                                                                                   Best Local Similarity 50.0
Matches 9; Conservative
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SMART; SM00356; ZnF_C3H
                                       HSSP; P38398; 1JM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
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Q8GX84
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2 SDYKFYEDANGTRDHKKG 19

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Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,

Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

Deng J.M., Hayashizaki Y., Hauan V.W., Lee J.M., Ishida J., Kamiya A.,

Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,

Seki M., Shinn P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,

Wu H.C., Yamadad K., Yu G., Yuan S., Shinozaki K., Ecker J.,

Theologis A., Davis R.W.;

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pama P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains I R.NG-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                             Eukaryoča; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similarity to zinc finger protein (Hypothetical protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BT000229; ANN15548 1; -...
GO; GO:000151; C:ubiquitin ligase complex; IEA.
GO; GO:0003676; F:ubiquitin ligase complex; IEA.
GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0016567; P:protein ubiquitination; IEA.
InterPro; IPR00051; Zif CCCH.
InterPro; IPR001841; Zif xing.
Pfam; PF00042; zf-CCCH; 1...
Pfam; PF00642; zf-CCCH; 1...
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SMART; SM00356; ZnF C3H1; 1.
PROSITE; PS00518; ZF RING 1; UNKNOWN 1.
PROSITE; PS500518; ZF RING 2; 1.
HYDOCHAE1CAl procein; Metal-binding; Zinc; Zinc-finger.
SEQUENCE 378 AA; 42518 MW; 142E4A6534BECA4D CRC64;
                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.9%; Score 47; DB 2; 50.0%; Pred. No. 55;
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378 AA
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                                                                                                                                             Hypotherical protein At5g06420.
Name=At5g06420,
Arabidopsis thaliana (Mouse-ear cress).
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PRT;
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01-MAR-2001 (TrEMBLrel. 16,
05-JUL-2004 (TrEMBLrel. 27,
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PRELIMINARY;
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nes 9; Conserv
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SEQUENCE FROM N.A.
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PRTT PORGI
P43158;
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                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. II. Sequence features of the regions of 1,044,062 bp covered by thirteen physically assigned Pl clones.";
      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                    SEQUENCE FROM N.A.
MEDLINE-98069011; PubMed-9405937;
Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MB4;
MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                          EMBL; AV081435, AAM67329.1; ...

REMBL; AV081435, AAM67329.1; ...

GO; GO:0000151; C:ubiquitin ligase complex; IEA.

GO; GO:0004842; F:ubiquitin ligase complex; IEA.

GO; GO:00048270; F:ubiquitin-protein ligase activity; IEA.

GO; GO:0008270; F:zinc ion binding; IEA.

R GO; GO:0016567; P:protein ubiquitination; IEA.

R InterPro; IPR001841; Znf_CCCH.

R Ffam; PP00097; zf-C3HC4; 1.

R Ffam; PP00642; zf-CCCH; 1.

R SWART; SW00184; RING; 1.

R SWART; SW00184; Znf_C3H; 1.

R PROSITE; PS00189; ZF_RING; 1.

R PROSITE; PS00189; ZF_RING; 2.

R HYPOTCHELCAI protein; Metal-binding; Zinc; Zinc-finger.

SEQUENCE 378 AA; 42460 MW; 173D71BBB8BA3FEED CRC64;
                                                                                                                                                                                       MEDLINE=22088475; PubMed=12093376; Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                      ς.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 2; Length 378;
Pred. No. 55;
?; Mismatches 7; Indels
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha-glucosidases, family 31 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Contains 1 RING-type zinc finger EMBL; AB006700; BAB08964.1; -- EMBL; AY087435; AAM67329.1: -
                                                                                                                                                                                                                                                    Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      751 AA.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.9%;
50.0%;
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Best Local Similarity 50.vv.,
Conservative
The 9; Conservative
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                                                                                                                                                     DNA Res. 4:291-300(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=119072;
                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       annotation.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@leb.sib.ch).
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                                                                                                                                                                                                                    .; IEA.
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-!- FUNCTION: Appears to be specific for arginine-containing peptide
-!- bonds. Possesses hemaglutinin activity.
-!- SIMILARITY: Belongs to peptidase family C10.
-!- CAUTION: It is uncertain whether Met-1 or Met-17 is the initiator.
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
A Tan H., Chen R., Wang J., Yu J., Yang H.;
Tan Complete sequence of the T. tengcongensis genome.";
Genome Res. 12:689-700(2001.
EMBL; AE012974; AAM23323.1;
EMBL; AE012974; AAM23323.1;
R GO; GO:0016787; F:hydrolase activity, hydrolyzing O-glycosyl . . .; I
R GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR000322; Glyco_hydro_31.
R Pfam; PF01055; Glyco_hydro_31; 1.
R PROSITE; PS000129; GLYCOSYL_HYDROL_F31_1; 1.
Complete proteome; Hydrolase.
Complete proteome; Hydrolase.
O SEQUENCE 751 AA; 88568 MW; 56AAFC74EDIACFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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   Lai X., Huang L., Dong X., Ma Y., Ling L., Yu J., Yang H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Thiol protease/hemagglutinin prtT precursor (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.9%; Score 47; DB 2; Length 751
52.6%; Pred. No. 1.2e+02;
52.6%; Pred. No. 1.2e+02;
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Pfam; PF01640; Peptidase C10; I.
PRINTS; PR00797; STREPTOFAIN.
ProDom; PD004169; Peptidase C10; 1.
Hemagglutinin; Hydrolase; Sīgnal; Thiol protease.
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"Isolation and characterization of the
general coding for protease activity";
Infect. Immun. 61:117-123(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M83096; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ATCC 53977;
MEDLINE=93114862; PubMed=8093357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671 KGRYVHYEDDGKTFDYKKG 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. [2]
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nes 9; Conservative
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. AEH1ORF131C.
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STRAIN=NRRL Y-1140;
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage Aehl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

REDIATE-95165001; PubMed=7806362;

RA Madden T.E., Clark V.L., Kuramiteu H.K.;

RA Madden T.E., Clark V.L., Kuramiteu H.K.;

RT Proteased-hemagallutinin gene: homology with streptococcal pyrogenic exotoxin B/streptococcal proteinsee.";

Infect. Immun. 63:238-247(1995).

DR REDIATE STS-942, ARB32891.1;

DR REDIATE STS-942, ARB32891.1;

DR ROO08234; F.cysteine-type peptidase activity; IEA.

GO, GO:0005509; P:pyroceolysis and peptidolysis; IEA.

DR GO, GO:0005509; P:pyroceolysis and peptidolysis; IEA.

DR PRINTS; PR00797; STREPTOFAIN.

DR PRINTS; PR00797; STREPTOFAIN.

DR PRINTS; PR00797; STREPTOFAIN.

DR Probom; PD004169; Peptidase C10; I.

Probom; PD004169; Peptidase C10; I.

DR Probom; PD004169; Peptidase C10; I.

PRODON; PD004169; Peptidase C10; I.

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                   Potential.
Potential.
Thiol protease/hemagglutinin prtT.
By similarity.
By similarity.
i, 45436EF832779323 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
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Petrov V., Nolan J., Bertrand C., Letarov A.V., Krisch H.M.,
Karam J.D.;
                                                                                                                                           43.9%; Score 47; DB 1; Length 868; ilarity 41.2%; Pred. No. 1.38+02; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.9%; Score 47; DB 2; Length 886;
41.2%; Pred. No. 1.4e+02;
iive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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                                                       868 Th
184 By
327 By
96444 MW;
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Best Local Similarity 41.27
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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ORFNames=AehlORF131c;
                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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ACT_SITE
SEQUENCE
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
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Kluyveromyces lactis (Yeast).
Eukaryota, Fungi; Ascomycota; Saccharomycetins; Saccharomycetels; Saccharomycete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses, dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
NCBL_TaxID=227470;
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                                                                                                                                                                                                                                                                                                                         Length 1211;
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                                                                                                                                                                                                                                                                            Score 47; DB 2; Length 121.
Pred. No. 1.98+02;
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"Aeromonas hydrophila phage Aehl complete genome ";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; Ax266303, AAQ17796.1; -.
Hypothetical protein.
SEQUENCE 1211 AA; 137634 MW; 6447E705BB2A9A88 CRC64;
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Petrov V., Nolan J., Karam J.D.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY266303, AAQ17796.1; -.
Hypothetical protein.
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
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Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boistrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicolski M., Oztaer S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolctin-Pukuhara M., Thierry A., Mincker P., Souciet J.L., Wicken D., Gaillardin C., Weissenbach J., Wicken P., Souciet J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NGS / Serotype c;
MEDLINE=91207143; PubMed=1982405;
Kelly C., Evans P., Ma J.K.C., Bergmeier L.A., Taylor W., Brady L.J.,
Lee S.F., Bleiweis A.S., Lehner T.;
"Sequencing and characterization of the 185 kDa cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kelly C., Evans P., Bergmeier L., Lee S.F., Progulske-Fox A.,
Harris A.C., Aitken A., Bleiweis A.S., Lehner T.;
"Sequence analysis of the cloned streptococcal cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
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STRAIN-UALS9 / ARCZ 700610 / Serctype c;
STRAIN-UALS9 / ARCZ 700610 / Serctype c;
MEDLINE-22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Cargon M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
Perretti J.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 2; Length 1467;
Pred. No. 2.4e+02;
2; Mismatches 3; Indels
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SEQUENCE 1467 AA; 165727 MW; F47CEDDD4F914998 CRC64;
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                                                                                                                                                                                                                                                                                                                                                       Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogen.";
Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002)
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28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1562 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell surface antigen I/II precursor.
Name=spaP; OrderedLocusNames=SMU.610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NG5 / Serotype c;
MEDLINE=90076473; PubMed=2687020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arch. Oral Biol. 35:338-388(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   43.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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                                                                                                                                                                                                                                                          Nature 430:35-44 (2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus mutans.
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Best Local Similarity
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SPAP_STRMU
ID SPAP_STRMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 X tandem repeats, Ala-rich.
3 X tandem repeats, Pro-ritch.
12 XTG sorting signal (Potential).
Pentaglycyl murein peptidoglycan amidated
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    -I- FUNCTION: Surface protein antigen implicated in dental caries.
    -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by

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threonine (Potential).
E -> Q (in Ref. 1 and 2).
NQAGETNGSIPV -> TKLERQMVHTI (in Ref. 1
                                                                                                                                                                                                                                                                       HSSP; P11657; 1JMM.
InterPro; IPR001899; Gram pos anchor.
InterPro; IPR001899; Gram pos anchor.
InterPro; IPR001899; Gram pos anchor;
Pfam; PF00766; Gram pos anchor; 1.
Pfam; PF00766; Strep_SA_rep; 7.
TIGREAMS; TIGR01167; LPXTG anchor; 1.
PROSITE; PSSO0477; GRAM POS_ANCHORING; 1.
Antigen; Cell wall; Complete protecome; Dental caries;
Direct protein sequencing; Peptidoglycan-anchor; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Probable)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell surface antigen I.
Cell surface antigen II (Probal
Removed by sortase (Potential)
Helical (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 1; Length 156 Pred. No. 2.5e+02; 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298B244E7A95F5D7 CRC64;
                                   (in Ref.
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D -> N (in Ref.
FKDGS -> LKNGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and 2)
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EMBL; AE014905; AANS8348.1; -.
PIR; S06839; S06839.
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ilarity 47.1%;
Conservative
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Matches 8; Conserv
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1307
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SIGNAL
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PAC STRMU
ID PAC STRMU
AC P11657;
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Teraco Y., Kawabata S., Hamada S.,
"Identification of Streptococcus mutans rgtB gene as a regulator og
glucosyltransferase expression.",
Submitted (MAR.2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB040534; BAC54564.1; --
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                                                                                                                                                                                                                                                             Length 1565;
                                                                                                                                                                                                                                                            / Match
Local Similarity 47.1%; Pred. No. 2.5e+02;
les 8; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                            829 829
1565 AA; 170781 MW; 4C3B05CB09D0C32A CRC64;
                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                         02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Protein antigen c.
                                                                                                                                                                                                                                                                                                                              PRT; 1565 AA.
                                                                                                                                                                                                                                                                                            3 DYKFYEDANGTRDHKKG 19
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
 Streptococcus mutans.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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 STRAIN=MT8148;
                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus.
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BAC54564;
Query Match
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Matches
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BAC54564
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
                                                                                                                                                                                                                                                                             LPXTG Sorting signal (Potential).
Pentaglycyl murein peptidoglycan amidated
threonine (Potential).
                                                         EMBL, X14490, CAA32652.1; -...
R PDB; 1JVM; X-ray; A=463-839.
R InterPro; IPR001899; Gram_pos anchor.
R InterPro; IPR001899; Strep SA_rep.
R InterPro; IPR0046; Gram_pos anchor.
R Pfam; PPF06696; Strep SA_rep; 1.
R PF06696; Strep SA_rep; 1.
R PR087TE; PS50847; GRAM POS ANCHORING; 1.
R PR087TE; PS50847; GRAM POS ANCHORING; 1.
R PLOSTE; PS50847; GRAM POS ANCHORING; 1.
R PLOSTE; PS50847; GRAM POS ANCHORING; 1.
R PLOSTE; PS50847; GRAM POS ANCHORING; 1.
R SIGNAL 1.
SIGNAL 1.
                                                                                                                                                                                                                                                            Removed by sortase (Potential)
                              Streptococcus mutans.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                                        Pac protein.
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1565
460
988
1536
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                                          Streptococcus.
NCBI_TaxID=1309;
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157
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1532
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                         Name=pac;
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PROPEP
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InterPro; IPR007653; SPC22.
InterPro; IPR010916; TONB_Box_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RSDYKFYEDANGTRDHK 17
                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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nes 8; Conserv
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NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                      rissum=Kidney;
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AAH67570;
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                   Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                      Score 47; DB 2; Length 1565;
Pred. No. 2.5e+02;
3; Mismatches 6; Indels
1565 AA; 170781 MW; 4C3B05C809D0C32A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bastos I.M.D., Santana J.M., Grellier P.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ496456; CAD42967.1; -.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR00470; Peptidase_S9A.
InterPro; IPR004106; Peptidase_S9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               698 AA; 77597 MW; A969F75872E45910 CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:85675.
                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Prolyl oligopeptidase (EC 3.4.21.26).
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Interpro; IPR000379; Ser estrs.
Pfam; PF00325, Peptidase_S9; 1.
PR0035; Peptidase_S9; 1.
PRINTS; PR00862; PR0LIGOPTASE.
PROSITE; PS00708; PRO_ENDOPEP_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                        698 AA
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                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                  : | | | | : | : | | | | 1381 EYNFYDDYDQTGDHYTG 1397
                                                                                 3,
                                                                                                                          3 DYKFYEDANGTRDHKKG 19
                                      Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                    rypanosoma brucei.
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SEQUENCE
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Q6HA27;
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064A2
10 064A2
AC 064A2
DT 05-JU
DE PROJY
DE PROJY
DE REMBL;
DR EMBL;
DR INTER
DR HYBNIT;
DR PFAM;
DR PRINT;
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TISSUE-Kidney,

KX Straubberg K.L., Febingold E.A., Grouse L.H., Derge J.G.,

KET STAUSPEZIANDES F.S., Wagner L., Shenmen C.M., Schuler G.D.,

KLAUSDER E., Febingold E.A., Grouse L.H., Derge J.G.,

KLAUSDER R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

KLAUSDER R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hale F.,

RA HORINS R.F., Jordan H., Moore T., Max S.I., Wang L.,

RA Brownstein M.J., Usdul T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Marek J.A., Gunaratne P.H.,

RA Allson D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RAIlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A.,

RAIlalon D.K., Marzuy D.M., Green E.D., Dickson M.C.,

Raleseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Raleseley R.W., Touchman J., Shavchenko Y., Bouffard G.G.,

RAZywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Jones S.J., Marza M.A.;

"Generation and initial analysis of more than 15,000 full-length human

"Tand mouse cDNA sequences.";
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunararne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A., Banchez A., Malting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF04573; SPC22; 1. — PROSTE; BS0430; TONB DEPENDENT_REC_1; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 180 AA; 20253 WW; 50FFD3C2B058A5AD CRC64;
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24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.0%; Score 46; DB 47.1%; Pred. No. 36; tive 4; Mismatches
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65 RKNYRHYENGNSFSEHEK 82
  1 RSDYKFYEDANGTRDHKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 38.9
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                      Q8W4G4;
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                                                                                                                                                    Q8W4G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q74LR8
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Matches
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Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,

Yamada K., Chan M.M., Chang C.H., Mallender E.K., Wong C., Wu H.C.,

Yu G., Yuan S., Carnincia P., Chen H., Cheuk R., Hayashizaki Y.,

Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,

Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,

Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,

Theologis A.,

Submitted (OCT-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopāis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Surosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone: MGF10 (Hypothetical protein At3g27700).
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                                                                                                                                                                                                              43.0%; Score 46; DB 2; Length 180;
47.1%; Pred. No. 36;
ive 4; Mismatches 5; Indels
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                                                                                  Strausberg R.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC067570; AAH67570.1; -.
                                                                                                                                                                         180 AA; 20253 MW; 50FFD3C2B058A5AD CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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EMBL, AB018114; BAB02694.1; --

EMBL, BT000780; AAN313919.1; --

GO; GO:0003676; F:nucleic acid binding; IEA.

InterPro; IPR00504; RNA_rec_mot.

InterPro; IPR00571; Znf_CCCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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124 KSKYFFFDDGNGLRANK 140
                                                                                                                                                                                                                                                                                                       1 RSDYKFYEDANGTRDHK 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00360; RRM; 1.
SMART; SM00356; ZNF_C3H1; 1.
PROSITE; PS50102; RRM; 1.
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                                                                                                                                                                                          Query Match
Best Local Similarity 47.1.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clones.";
DNA Res. 7:131-135(2000).
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                                                                                                                                                  Hypothetical protein.
SEQUENCE 180 AA; 2
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Best Local Similarity
Matches 7; Conserva
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                                        SEQUENCE FROM N.A.
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                                                                TISSUE=Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 30
O9LVX1
10 09LVX2
AC 091LVX
AC 091LVX
AC 091LVX
DT 01-0C

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SOUTHWICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,

A Cheuk R., Chung W.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Bakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Bakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Bakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Bakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Bakuri J., Theologis A., Davis R.W.,

Co., Gologologis F. Pincleic acid binding; IEA.

InterPro; IPRO0571; Znf_CCCH.

InterPro; IPRO0571; Znf_CCCH.

R. Fran, PPRO051; Znf_CCH; 1.

SWART; SMO0360; RRM; 1.

R. SMART; SMO0360; RRM; 1.
                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids,
eurosids II; Brassicales; Brassicaceae, Arabidopsis.

NCBI_TaxID=3702;
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PubMed=14966310;
Pridence R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pridence R.C., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
"The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533.";
Emcrobacillus Johnsonii NCC 533.";
EMBL; AE017200; AAS08097.1; -.
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Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                   Last annotation update)
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Last annotation update)
                                                                                                             Last sequence update)
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Pred. No. 2e+02;
5; Mismatches
   908 AA.
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                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence
1-MAR-2004 (TrEMBLrel. 26, Last annotativ
Hypothetical protein At3g27710; MGF10.11.
Name=At3g27710/MGF10.11;
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PRT;
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RKNYRHYENGNSFSEHEK 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.0%;
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01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ListiList; LIN2540;
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Local 7; Conserv
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SEQUENCE 1090 AJ
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Q8Y4J2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8Y4J2
            RAPARAPA
BARAPA
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InterPro; IPR000421; FAS8_C.
InterPro; IPR003961; FN III.
InterPro; IPR008979; Gal_bind_like.
InterPro; IPR008979; Gal_bind_like.
InterPro; IPR008979; Gal_bind_like.
InterPro; IPR00032; Glyco_hydro_31.
Ffam; PP00041; Fins.
Pfam; PP00041; Fins.
Pfam; PP01055; Glyco_hydro_31; 1.
Pfam; PP01055; Glyco_hydro_31; 1.
PROSITE; PS50831; FN3; 1.
PGOMPLE; Protecone; Hypothetical protein.
SEQUENCE 1019 AA; 115270 MW; 722BEEF0B85CB032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.0%; Score 46; DB 2; Length 1019; 47.4%; Pred. No. 2.3e+02; ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.0%; Score 46; DB 2; Length 1019; 47.4%; Pred. No. 2.3e+02; tive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TaxID=33959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1019 AA; 115270 MW; 722BEEF0B85CB032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE-21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635 KSSAILYEDDNQTNDYEKG 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| | | | | | ::|| 635 KSSAILYEDDNQTNDYEKG 653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 47.4%;
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MRA-2004 (TrEMBLrel. 26,
1-in2540 protein.
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PubMed=14966310;
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AAS08097
ID AAS0808
AC AAS08
DT 02-MA

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0928J2
10 0928J3
AC 0928J
DT 01-DE
DT 
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
A Charbit A., Chetouraif F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Falhi H., Garcia-del Portillo F., Garrido P.,
Aduler L.-M., Kaeret U., Kreft J., Kuhn M., Kunst F., Mard G., Jackson D.,
Andueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Dhaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Azquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.";
Science 294:849-852(2001).
R EMBL, AL591981; CAD00524.1; -.
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Brian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
Adutter L., Gobbel W., Gomez-Lopez N., Haif T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreit J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordeise G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simose N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.";
Science 294:849-852(2001).
R. EMBL, ALS56172; CAC97767.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0030246; F:carbohydrate binding; IEA.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
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GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
GO:0005975; P:carbohydrate metabolism; IEA.
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Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
NOBI_TaxID=1639,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1090 AA; 121745 MW; 5294EF5A0327ECBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.0%; Score 46; DB 2; Length 109
63.6%; Pred. No. 2.5e+02;
ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005084; CBM 6.
InterPro; IPR008979; Gal_bind like.
InterPro; IPR00322; Glyco_hydro_31.
InterPro; IPR007110; Ig-like.
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MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01055; CBM 6; 1.
Pfam; PF01055; Glyco_hydro_31; 1.
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Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Feterson J., White O., Nelson W.C., Nierman W.C., Madupu H.J.,
Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
Haft D.H., Selengut J., Van Aken S., Khouri H., Fedorova N.,
Forbeger H., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.; and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species.";
Nucleic Acids Res. 32:2386-2395(2004).
  Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1091 AA; 121658 MW; 359049E0243DDB8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 63.0
                          Listeria monocytogenes.
NCBL_TaxID=26569;
                                                                                                                     STRAIN=4b F2365;
                                                                                                                                          PubMed=15115801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome VII
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ID YG3V_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15115801; DOI=10.1093/nar/gkh562;
PubMed=15115801; DOI=10.1093/nar/gkh562;
Nelson K.E., Foute D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
Peterson J.D., White O., Nelson W.C., Nierman W.C., Beanan M.J.,
Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
Haft D.H., Selngut J., Van Aken S.E., Khouri H.M., Fedorova N.,
Forberger H.A., Tran B., Kathariou S., Wonderling L.D., Uhlich G.A.,
Bayles D.O., Luchansky J.B., Fraser C.M.;
"Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome componiants of this species.";
Nucleic Acids Res. 32:2386-2395(2004).
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                                                                                                                                                                                     Length 1091;
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Listeria monocytogenes (serotype 4b / strain F2365).
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                          1091 AA; 121698 MW; 55FC3969F472DCDE CRC64;
                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121658 MW; 359049E0243DDB8B CRC64;
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10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                     Score 46; DB 2; 1
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005084; CBM 6.
InterPro; IPR008979; Gal_bind like.
InterPro; IPR008979; Gal_bind like.
InterPro; IPR001329; Glyco_hydro_31.
InterPro; IPR07110; Ig-like.
Pfam; PF01452; CBM 6; 1.
Complete proteome; Hydrolase.
SEQUENCE 1091 AA; 121658 WW; 35904;
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LMOF2365 2419.
Listeria monocytogenes str. 4b F2365.
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InterPro; IPR008979; Gal bind like.
InterPro; IPR000322; Glyco hydro_31.
InterPro; IPR007110; Ig-like.
                                                                  Pfam; PF03422; CBM 6; 1.
Pfam; PF01055; Glyco hydro 31; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosyl hydrolase, family 31
                                                                                                                                                                                       43.0%;
63.6%;
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Best Local Similarity 63.57
Best Local 7; Conservative
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Best Local Similarity 63.67
Conservative
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864 SEYSFYDDVNG 874
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864 SEYSFYDDVNG 874
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                                                                                                                                                                                                                                                                                2 SDYKFYEDANG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SDYKFYEDANG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=265669;
                                                                                                                     Complete proteome. SEQUENCE 1091 AA
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AAT05185;
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DT 10-M
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Length 1091;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                             ö
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
"Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical 39.6 kDa protein in GTR2-KRE11 intergenic region.
OrderedLocusNames=YGR165W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z72950, CAA97189.1; -. PIR; S64476; S64476; S64476; S64476; S64477; -. Germonline; 141477; -. Germonline; 141477; -. Go. S0003397; Yall65W. GO; GO: 0005763; C: mirochondrial small ribosomal subunit; IPI. GO; GO: 00003735; F: structural constituent of ribosome; IPI. GO; GO: 0000960; P: searobic respiration; IEP. GO; GO: 0006412; P: protein biosynthesis; IC.
43.0%; Score 46; DB 2; Length 109
63.6%; Pred. No. 2.56+02;
".marches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 345 AA, 39575 MW; 4E363E30F5056329 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97435481; PubMed=9290212;
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864 SEYSFYDDVNG 874
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DB 1; Length 345;

42.5%; Score 45.5;

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C STRAIN=1216 / ATCC 49652 / DSM 12025;

X MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;

Bisen J.A., Nelson K.E., Pauleen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., DeBoy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,

A Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,

A Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,

A Radune D., Vamathevan J.J., Khouri H.M., White O., Gruber T.M.,

A Ketchum K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaeroble, green-sulfur bacterium.",

I Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
                                                         Gaps
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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42.5%; Score 45.5; DB 2; Length 381;
Best Local Similarity 62.5%; Pred. No. 97;
Matches 10; Conservative 1; Mismatches 2; Indels 3
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Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AVIGAT41, AAN7511.1;
GO; GO: 0005524; F.APP binding; IEA.
GO; GO: 0003968; F:APP binding; IEA.
InterPro; IPR00208; Flavi NS5.
InterPro; IPR002087; Finaling:
Pfam; PF00972; Flavi NS5; 1.
Pfam; PF01728; FtBJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlorobium tepidum.
Bacteria, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae,
                                                    5; Indels
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SEQUENCE 381 AA; 42377 MW; 2CDDDEF72C48C479 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Hypothetical protein CT2147.
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Last annotation update)
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Best Local Similarity 40.7%; Pred. No. 87;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                               304 RSQYKFTNAKVGKVGYRYGSGNRDNKK 330
                                                                                                                                          1 RSDYKF-----YEDANGTRDHKK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=CT2147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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01-MAR-2003 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
NS5 protein (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002
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08848
AC 08848
DT 01-MAD
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00RAK9
AC QBRAK
AC QBRAK
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DT 01-0C
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Length 890;
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890
100683 MW; 199C3122BDF4382B CRC64;
                                                        Query Match
42.5%; Score 45.5; DB 2;
Best Local Similarity 64.7%; Pred. No. 2.4e+02;
Matches 11; Conservative 0; Mismatches 3;
                                                                                                                                                                                         Search completed: November 24, 2004, 09:29:01
Job time : 90.3587 secs
                                                                                                                                                 248 KFEEDANLSSGTRAHSK 264
                                                                                                                      5 KFYEDAN---GTRDHKK 18
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein November 24, 2004, 09:11:44 Run on:

; Search time 15.6957 Seconds (without alignments) 116.473 Million cell updates/sec

US-09-719-379A-5 Title: Perfect score:

1 RSDYKFYEDANGTRDHKKG 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

seq length: 0 seq length: 200000000 88 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR Database

1: pirl: * 2: pirl: * 3: pirl: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	probable outer mem	putaive outer memb	hypothetical prote	probable zinc fing	cysteine proteinas	surface antigen sp	surface antigen pa	glycosidase homolo	glycosidase homolo	hypothetical prote	DNA-directed RNA p	diadenosine tetrap	protein T1F9.22 [i	hypothetical prote	protein T04All.11	n	N		R10H1		Y6B3B			protein Y45F10D.1	88.6K hypothetical	position-specific	hypothetical prote	hypothetical prote	_
0011111100	ΩI	E85729	D90888	T28872	G86143	T10890	806839	S04729	AG1749	AF1380	S64476	C90126	G84201	G96638	T20776	G88864	S27787	E87901	E87969	G88210	H89382	F87991	H87720	D88198	A88892	C86406	A29637	T18472	T22942	D86246
	DB	7	~	7	~	7	Н	-	•	N	~	~	~	•	~	~								~						
	Query Match Length	366	366	997	304	988	1561	1565	1090	1001	345	339	142	303	326	329	329	329	329	329	329	329	329	329	329	786	1394	2269	995	298
æ	Query Match	44.4	44.4	44.4	43.9	43.9	43.9	43.9	43.0	43.0	42.5	42.1	41.1	41.1	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	39.7	39.3
	Score	47.5	47.5	47.5	47	47	47	47	46	46	45.5	45	44	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	42.5	42
	Result No.	1	7	٣	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

hypothetical prote	D-3-phosphoglycera	tRNA (guanine N-1)	tRNA (guanine-N1)-	hypothetical prote	glucosidase BH0704	repetin - mouse	signal peptidase (	hypothetical prote	conserved hypothet	hypothetical prote	ORF MSV072 hypothe	hypothetical prote	hypothetical prote	t-complex protein	hypothetical prote
T29384	G96901	F86505	C72117	A83691	H83737	T30251	S22412	H69265	G82939	S51815	T28233	D89943	T30402	E90086	A70120
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301	30	m	m	•		_									
			39.3			38.8	38.3	38.3		38.3		38.3	38.3	38.3	38.3
			2 39.3		39.3	41.5 38.8 1		41 38.3		41 38.3		41 38.3	41 38.3	41 38.3	41 38.3

## ALIGNMENTS

probable outer membrane porin protein 2239 [imported] - Escherichia coli (strain O157:H C;Species: Escherichia coli di Saccession: E85129 [inter, L.; Burkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 400, 529-531, 2001
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85729
A;Accession: E85729
A;Accession: E85729
A;Accession: E85729
A;Residues: 1-366 <STO>
A;Residues: 1-366 <STO>
A;Residues: UNIPROT:QBXASO; GB:AE005174; NID:g12515212; PIDN:AAG56297.1; GSPDB:G A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics: 2013

A,Gene: Z2239 C,Superfamily: outer membrane protein phoE

Length 366; DB 2;

Gaps 1; Indele 2; Query Match
44.4%; Score 47.5; D
Best Local Similarity 62.5%; Pred. No. 13;
Matches 10; Conservative 3; Mismatches

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|:| | | | ||:||:| 80 DFKGYNDEANGSRDNK 95 g

3 DYKFYED-ANGTRDHK 17

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RESULT 2

Cybecies: Escherichia coli Cybecies: Escherichia coli Cybecies: Escherichia coli Cybecies: Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 CyAccession: D90888 RyHayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A, Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno A, Steference number: A99629; MUID:21156231; PMID:11258796 A, Steadus: preliminary A, Steadus: 1-366 < HAX> A, Residues: 1-366 < HAX> A, Residues: 1-366 < HAX> A, Experimental source: strain O157:H7, substrain RIMD 0509952

A,Gene: BCB2076 C,Superfamily: outer membrane protein phoB

DB 2; Length 366; 44.4%; Score 47.5; Query Match ó

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C;Accession: T10890
Myadden, T.E; Cark, V.L.; Kuramitsu, H.K.
Infect. Immun. 63, 238-247, 1995
A;Title: Revised sequence of the Porphyromonas gingivalis prtT cysteine protease/hemaggl
A;Title: Revised sequence of the Porphyromonas gingivalis prtT cysteine protease/hemaggl
A;Reference number: Z17199; MUID:95105001; PMID:7866362
A;Accession: T10890
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surface antigen spaP precursor - Streptococcus mutans

U;Alernate names: antigen I/II

C;Spaces Streptococcus mutans

C;Date: 03-Mar-1994 #text_change 09-Jul-2004

C;Accession: S06839; A60339; A60661

C;Accession: S06839; A60339; A60661

C;Accession: Sober Solution Solutio
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A;Residues: 1-1561 <KEL>
A;Cross-references: UNIPROT:P23504; EMBL:X17390; NID:g47266; PIDN:CAA35253.1; PID:g47267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: parts of this sequence, including the amino ends of the mature proteins, were considered this sequence, including the amino ends of the mature proteins, were considered to the sequence, including the sequence of S.F.; Arch. Oral Biol. 35(Suppl.), 33S-388, 1990
A;Itle: Sequencing and characterization of the 185 kDa cell surface antigen of Streptoc A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
A;Contents: annotation
A;Title: Conservation of the gene encoding streptococcal antigen I/II in oral streptococcal, A;Reference number: A60339; MUID:91310321; PMID:1855988
                                                       / hemagglutinin protein - Porphyromonas gingivalis
                                                       cysteine proteinase (EC 3.4.22.-) / hemagglutinin protein - Porphyromonas g:
C;Species: Porphyromonas gingivalis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-886 <MAD>
A;Cross-references: UNIPROT:Q53481; EMBL:S75942; NID:g913136; PID:g913137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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K:Keywords: duplication; glycoprotein; transmembrane protein
F:1-38/Domain: signal sequence #status predicted <SIG>
F:39-1561/Product: surface antigen spaP.I #status predicted <MATI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB 2; Length 886;
Pred. No. 35;
3; Mismatches 7; Indels
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illarity 41.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
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GR6143

probable zinc finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86143
A;Authors: Hujdes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Huizar, L.; Juh, S.X.; Liu, Z.A.; Lucs, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.; W.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Retus: preliminary
A;Molecule type: DNA
A;Reatus: preliminary
A;Molecule type: DNA
A;Reatus: cferences: UNIPROT:Q9LN19; GB:AE005172; NID:g9665151; PIDN:AAF971335.1; GSPDB:GN
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein R04E5.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28872
R;Miller, N.
Bubmitted to the EMBL Data Library, December 1995
A;Posecription: The sequence of C. elegans cosmid R04E5.
A;Reference number: Z20535
A;Accession: T28872
A;Resion: T28872
A;Resion: T28872
A;Resion: T28872
A;Resion: T2897 *ML>
A;Resions: 1-997 *ML>
A;Resions: 1-907 *ML>
A;Resions: 1
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50.0%; Pred. No. 12;
ive 2; Mismatches 7; Indels
                                                            Indels
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A;Introns: 216/3; 234/3; 255/2; 305/1; 669/3; 891/1; 986/2
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Local Similarity 62.5%; Pred. No. 33;
hes 10; Conservative 2; Mismatches
62.5%; Pred. No. 13; tive 3; Mismatches
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80 DFKGYNDEANGSRDNK 95
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Best Local Similarity 62.5
Matches 10; Conservative
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Best Local Similarity
Matches 9; Conserv
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Matches

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Glycosidase homolog lmo2446 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF1380
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
Joninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma-Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q8Y4J2; GB:NC_003210; PIDN:CAD00524.1; PID:g16411934; GSPDB:
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A;Residues: 1.345 «RIE»
A;Cross-references: UNIPROT:P53292; EMBL:Z72950; NID:g1323289; PID:e243551; PID:g1323290
A;Experimental source: Btrain S288C
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N,Alternate names: hypothetical protein G7050
C,Species: Saccharomyces cerevisiae
C,Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
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DNA-directed RNA polymerase 40k chain [imported] - Guillardia theta nucleomc
C.Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
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      Gaps
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      Indels
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R;Rteger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M. Bubmitted to the Protein Sequence Database, May 1996
A;Reference number: $64071
A;Accession: $64476
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Pred. No. 61;
2; Mismatches
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42.5%; Coore 45.5; EBest Local Similarity 40.7%; Pred. No. 24; Matches 11; Conservative 2; Mismatches
      Mismatches
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Best Local Similarity 63.6%;
Matches 7; Conservative
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A;Map position: 7R
         Conservative
                                                                                                                          864 SEYSFYDDVNG 874
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                                                                 2 SDYKFYEDANG 12
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      7;
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         Matches
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AG1749
Glycosidaee homolog lin2540 [imported] - Listeria innocua (strain Clip11262)
C; Species: Listeria innocua
C; Date: 27-Nov-2001 #text_change 09-Jul-2004
C; Accession: AG1749
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 4849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Residues: 1-1090 <GLA>
A; Residues: 1-1090 <GLA>
A; Residues: 1-1090 <GLA>
A; Residues: U. Discource: Strain Clip11262
C; Genetics:
C; Genetics: Lin2540
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A.Residues: 1-1565 < OKX>
A.Residues: 1-1565 < OKX>
A.Residues: 1-1565 < OKX>
A.Cross-references: UNIPROT:P11657; EMBL:X14490; NID:g47247; PIDN:CAA32652.1; PID:g47248
A.Cross-references: UNIPROT:P11657; EMBL:X14490; NID:g47247; PIDN:CAA32652.1; PID:g47248
A.Fore: part of this sequence, including the amino end of the mature protein, was confir C.Superfamily: surface antigen spaP
C.Superfamily: surface antigen; transmembrane protein
F.1-38/Domain: signal sequence #status predicted <SIG>
F.1-38/Domain: signal sequence #status gredicted <SIG>
F.39-1565/Product: surface antigen pac #status experimental <MAT>
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C;Species: Streptococcus mutans
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S04729
R;Okahashi, N.; Sasakawa, C.; Yoshikawa, M.; Hamada, S.; Koga, T.
Mol. Microbiol. 3, 673-678, 1989
A;Tille: Molecular characterization of a surface protein antigen gene from the A;Reference number: S04729; MUID:89343654; PMID:2761390
                                                                                                                                                                                                                                                                                                             Gaps
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P;383-407/Domain: spaP alanine-rich repeat <AR9>
P;408-426/Domain: spaP alanine-rich repeat <AR10>
F;440-464/Domain: spaP alanine-rich repeat <AR11>
F;840-885/Domain: spaP proline-rich repeat <PR1>
F;840-983/Domain: spaP proline-rich repeat <PR2>
F;985-963/Domain: spaP proline-rich repeat <PR2>
F;985-963/Domain: spaP proline-rich repeat <PR2>
F;997-1561/Product: surface antigen spaP.II #status predicted <MAT2>
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60;
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3; Mismatches
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Pred. No.
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1377 EYNFYDDYDQTGDHYTG 1393
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Matches 8; Conservative
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Best Local Similarity
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Wed Nov 24

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A; Accession: G96638
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-303 <STO>
A; Cross-references: UNIPROT:064791; GB: AE005173; NID: g3056601; PIDN: AAC13912.1; GSPDB: GNG
C; Genetics:
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elea.A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:062151; EMBL:Z81500; PIDN:CAB04094.1; GSPDB:GN00023; CESP:F1
A;Experimental source: clone F11D11
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Superfamily: Caenorhabditis transposon Tcl hypothetical 32K protein
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Pred. No. 54;
5; Mismatches
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A;Molecule type: DNA
A;Residues: 1-326 <WIL>
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R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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R;Mortimore, B.; Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19323
                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 44; DB 46.7%; Pred. No. 36; Live 3; Mismatches
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Best Local Similarity 46...
Rest Local 7; Conservative
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Best Local Similarity 37.5:
Matches 9; Conservative
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C;Superfamily: syntaxin
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A;Molecule type: DNA
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A; Introns: 136/3
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C90126
R;Douglas, S; Zauner, S; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Recession: C90126
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-339 < DOUS
A;Cross-references: UNIPROT:Q98S79; GB:AF083031; NID:g13794326; PIDN:AAK39703.1; GSPDB:C
C;Genetics:
A;Gene: rps
A;Gene: rps
A;Gene: rps
A;Gene: rps
A;Gene: rps
C;Keywords: nucleomorph
C;Keywords: nucleomorph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-142 <STO>
A;Cross-references: UNIPROT:Q9HS29; GB:AE004437; NID:g10580041; PIDN:AAG18979.1; GSPDB:G
C;Genetics:
A;Gene: apa
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A;Status: preliminary
A;Molecule type: DNA
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A;Tille: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A75000; MID:99069613; PMID:9851916
A;Reference number: A75000; MID:9906613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele. A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A;Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A;Ro00; MIID:99069613; PMID:981316

A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C_ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.45, 'L', 47-316, 'F', 318-329 <WI4>
A;Residues: 1.45, 'L', 47-316, 'F', 318-329 <WI4>
A;Cross-references: EMBL:AL021492; PIDN:CAA16380.1; GSPDB:GN00022; CESP:Y45F10D.1
A;Experimental source: clone Y45F10D
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C;Species: Caenorhabditis elegans
C;Pate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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A,Introns: 79/2; 139/3
C,Superfamily: Caenorhabditis transposon Tcl hypothetical 32K protein
C,Keywords: DNA binding; nucleus
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55;
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A;Gene: CESP:F56A6.3; CESP:Y6B3B.8; CESP:Y45F10D.1
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Pred. No. 55;
5; Mismatches
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A,Gene: CESP:T02G5.5; CESP:F38A1.2
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Best Local Similarity 37.5%;
Matches 9; Conservative
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nes 9; Conserv
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A;Introns: 139/3
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C;Species: Caenorhabditis elegans
C;Date: 17-Apr-1993 #text_change 09-Jul-2004
C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Date: 17-Apr-1993 #sequence revision 17-Apr-1994; T27325; T26932
R;Du, Z.; Ainscough, R.; Berks, M.; Craxton, M.; Coulson, A.; Dear, S.; Durbin, R.K.; Gr
Qiu, Q.; Shownkeen, R.; Staden, R.; Sulston, J.; Thierry-Mieg, J.; Thomas, K.; Waterston Quin C; Shownkeen RMBL Data Library, October 1991
A;Description: Sequence of the C. elegans cosmid B0303.
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;Cross-references: EMBL:U41105; NID:g1086772; PID:g1086778; PIDN:AAA82401.1; CESP:T02G5
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A;Molecule type: DNA
A;Residues: 1-316, FV, 318-329 < MUR>
A;Residues: 1-316, FV, 318-329 < MUR>
A;Cross-references: EMBL:AF067217; PIDN:AAC17016.1; GSFDB:GN00019; CESP:F56A6.3
A;Experimental source: strain Bristol N2; clone F56A6
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A;Cross-references: EMBL:AL032655; PIDN:CAA21724.1; GSPDB:GN00019; CESP:Y6B3B.8
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A,Residues: 1-316,'F',318-329 <WIL>
A,Cross-references: EMBL:Z80213; PIDN:CAB02260.1; GSPDB:GN00022; CESP:F38A1.2
A,Experimental source: clone C09E9
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A; Accession: T21396
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Relatious: 1-316, FF, 318-329 < WIZ>
A; Redidues: 1-316, FF, 318-329 < WIZ>
A; Redidues: Lasiones: EMBL: 2281535; PIDN: CAB04359.1; GSPDB: GN00022; CESP: F38A1.2
A; Experimental source: clone F38A1
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A;Residues: 1-29 <DUZ>
A;Residues: 1-29 <DUZ>
A;Cross-references: UNIPROT:P34257; EMBL:M77697; NID:g156188; PID:g156196
B;Muxray, J.; Rohlfing, T.; O'Neal, D.; Wilson, R.
submitted to the EMBL Data Library, May 1998
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A; Accession: T33080
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A;Molecule type: DNA
A;Residues: 1-86,'F',88-316,'F',318-329 <WI3>
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Akeference number: 219076
Akecession: 119124
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Aketeus: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, January 1998
A;Reference number: 220288
A;Accession: T26932
          llarity 37.5%; Pred. No. 55;
Conservative 5; Mismatches
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             Best Local Similarity
Matches 9; Conserv
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C;Accession: F87991
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
Science 287, 2012-2018, 1998
A;Title: Genome sequence the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleA;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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C; Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein
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C,Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein
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C;Superfamily: Caenorhabditis transposon Tcl hypothetical 32K protein
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Pred. No. 55;
5; Mismatches
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
                                                     Score 43; DB 2
Pred. No. 55;
5; Mismatches
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                                                                                                                                                                                                      223 RKDFRFQQDNATIHVSNSTRDYFK 246
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                                                                                                                                                                         1 RSDYKFYED-----ANGTRDHKK 18
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milarity 37.5%;
Conservative 5
                                                        Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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A,Status: preliminary
A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: Y6B3B.8
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Best Local S:
Matches 9
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RESULT 19

GR8210

protein R10H1.3 [imported] - Caenorhabditis elegans
N;Alternate names: protein T20H12.2
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: G88210; B88116
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nemarode C. elegans: a platform for investigating biolog
A;Reference number: A'5000; MUID:9965813; PMID:981916
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G88210
A;Accession: G88210
A;Accession: G88210
A;Accession: G88210
A;Accession: G88210
A;Accession: G88210
A;Accession: BNA
A;Residues: 1-239 &STO>
A;Cross-references: UNIPROT:Q21913; GB:chr_II; PIDN:C46711.1; PID:g726401; GSPDB:GN0020
A;Accession: B88116
A;Accession: B88116
A;Accession: BRA
A;Residues: 1-329 &STO>
A;Cross-references: GB:chr_II; PIDN:AB66089.1; PID:g2315641; GSPDB:GN0020; CESP:T20H12.
C;Generics: R10H1.3; T20H12.2
A;Generics: R10H1.3; T20H12.2
A;Map position: 2
C;Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: O-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H99382
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele
A;Accession: H89382
A;Status: preliminary
A;Accession: H89382
A;Status: preliminary
A;Residues: 1-129 csTO>
A;Croos-references: UNIPROT:045997; GB:chr_V; PIDN:CAB04983.1; PID:g3881558; GSPDB:GN000
C;Genetics:
A;Acne: zx218.2
A;Map position: 5
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                          C;Genetics:
A;Gene: Y47H9C.3
A;Map position: 1
C;Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein
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Pred. No. 55;
5; Mismatches 4; Indels
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larity 37.5%; Pred. No. 55;
Conservative 5; Mismatches
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predicted using Genefinder
                                                                                                                                                                   Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
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Matches 9; Conserv
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  A;Note:
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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C..
C.A.; Li, J.H.; Li, Y.; Liu, X.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rodiey, T.; Rweley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT: Q9C7E7; GB: AE005172; NID: g11024878; PIDN: AAG26962.1; GSPDB:G:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 51, 929-940, 1987
A;Title: The Drosophila PS2 antigen is an invertebrate integrin that, like the fibronect
A;Reference number: A29637; MUID:88080480; PMID:2961459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-1394 <BOGS
A; Residues: 1-1394 <BOGS
A; Residues: 1-1394 <BOGS
A; Residues: 1-1394 <BOGS
A; Residues: 1-1394 U.L.; Wilcox, M.; Kafatos, F.C.
Cell 59, 185-195, 1989
A; Title: Developmentally regulated alternative splicing of Drosophila integrin PS2 alpha
A; Reference number: A33335; MUID:90003228; PMID:2507168
A; Accession: A33335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         position-specific antigen 2 alpha chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
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C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Keywords: cell adhesion; cytoskeleton; duplication; heterodimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1394;
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Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 10; Conservative 1; Mismatches 7; Indels
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40.2%; Score 43; DB 2; 1
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 1; Mismatches 8.
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A;Molecule type: DNA
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submitted to the EMBL Data Library, November 1998
A;Reference number: 218937
A;Accession: T18472
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Cell 51, 929-940. 1987
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A; Residues: 201-301 <BRO>
                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-786 <STO:
                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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                                                              protein T02G5.5 [imported] - Caenorhabditis elegans

C;Species Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D88198
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematcode C. elegans: a platform for investigating biolog A;Title: Genome sequence wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein Y45F10D.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: A88892
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID: 99065613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_eleA;Note: see websites appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: A88892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 < STO>
A;Cross-references: UNIPROT: O62475; GB:chr_IV; PIDN:CAA16380.1; PID:g3880993; GSPDB:GNOGA;Note: predicted using Genefinder
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106406
10. Goldenor  
10. Species: Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C8606
R;Theologis, A.; Bcker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huizar, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q22104; GB:chr_II; PIDN:AA82401.1; PID:g1086778; GSPDB:GN000
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A;Map position: 4
C;Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein
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Pred. No. 55;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 329;
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Pred. No. 55;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

8est Local Similarity 37.5%; Pred. No. Matches 9; Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 RKDFRFQQDNATIHVSNSTRDYFK 246
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Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-329 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: D88198
A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2
C; Superfamil.
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39.3%; Score 42; DB 2; ilarity 41.2%; Pred. No. 72; Conservative 3; Mismatches 7
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TRDHKKG 19
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                           KFYEDANGTRDHKKG 19
                                                                     30 KFFEDVENVKDDMKG 44
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Best Local Similarity
Matches 10; Conserv
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Matches 7; Conserv
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession. D86246
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, Y.; Lin, X.; Liu, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:P90897; EMBL:Z81094; PIDN:CAB03153.1; GSPDB:GN00023; CESP:F5
A,Experimental source: clone F58G11
            A;Cross-references: UNIPROT:077360; EMBL:AL008970; NID:e1407852; PID:e1332566; PIDN:CAALA;Genetics:
A;Gene: C0440c
A;Amp position: 3
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A;Crose-references: UNIPROT:Q9SXB0; GB:AE005172; NID:g5734739; PIDN:AAD50004.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F58G11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22942
R;Percy, C.
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42.1%; Pred. No. 1.9e+02;
Live 5; Mismatches 3; Indels
                                                                                                                                        Score 43; DB 2; Length 2269;
Pred. No. 3.5e+02;
3; Mismatches 4; Indels
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46.7%; Pred. No. 71;
ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19640
A;Accession: T22942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-995 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 5
A;Introns: 79/1; 195/1; 642/1; 678/2; 796/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 RNDYRSQQD---SRDHRSG 272
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                                                                                                                                          40.2%;
                                                                                                                                                                                                                                                                         182 YKFYDDKNEKKSNK 195
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                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 7; Conservative
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Best Local Similarity 46.7
Matches 7; Conservative
A;Residues: 1-2269 <LAW>
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A, Status: preliminary
A, Molecule type: DNA
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C:Superfamily: 89
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Matches
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A;Residues: 1-301 <GEI>
A;Cross-references: UNIPROT:Q21319; EMBL:U55857; PIDN:AAA98029.1; GSPDB:GN00022; CESP:KO
A;Experimental source: strain Bristol N2; clone K08D10
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Synolling, J.; Breton, G.; OmelChenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bally, M.J.; Bentett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Tille: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A;Reference number: A96900; MUID:21359325, PMID:21359325
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A;Residues: 1-305 <KUR>
A;Cross-references: UNIPROT:Q97N23; GB:AE001437; PIDN:AAK78002.1; PID:g15022834; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0015
C;Superfamily: phosphoglycerate dehydrogenase
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hypothetical protein KO8D10.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D-3-phosphoglycerate dehydrogenase [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
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A;Introns: 73/3; 193/3; 256/1
C;Superfamily: Caenorhabditis elegans hypothetical protein K08D10.7
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                                                                                                                                           RiGeisel, C.; Bradshaw, H. submitted to the EMBL Data Library, April 1996 A;Description: The sequence of C. elegans cosmid KO8D10. A;Reference number: 220616
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39.3%;
ilarity 72.7%;
Conservative
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ilarity 41.7%;
Conservative
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Best Local Similarity
7; Conserva
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: H83737
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: R86505
A;Accession: R86505
A;Accession: Paciminary
A;Molecule type: DNA
A;Residues: 1-361 <670>
A;Residues: 1-361 <670>
A;Residues: 1-361 <670>
A;Cross-references: UNIPROT:Q92964; GB:BA000008; NID:g8978491; PIDN:BAA98328.1; GSPDB:GNA;Experimental source: strain J138
A;Experimental source: strain J138
A;Genetics:
A;Genetics:
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hypothetical protein BH0329 [imported] - Bacillus halodurans (strain C-125)

hypothetical protein BH0329 [imported] - Bacillus halodurans

C;Species Bacillus halodurans

C;Species Bacillus halodurans

C;Accession: A83691

R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira

Nucles Caids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUD:20512582; PMID:11058132

A;Accession: Bacilminary

A;Molecule type: DNA

A;Residues: 1-423 <STO>

    Chlamydophila pneumoniae (strain

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A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tRNA (guanine-N1)-methyltransferase CP0656 [imported] - Chlamydophila pneumoniae (strair C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: C72117; D81553
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
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                                                                                                                                                                                                                                                                                                            Length 361;
                                                                                                                                                                                                                                                                                                                                                      6; Indels
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5
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Pred. No. 85;
2; Mismatches
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                                                                                                                                                                                                                                                                                              39.3%; Score 42;
illarity 50.0%; Pred. No.
Conservative 2; Mismatr
                                                                                                                                                                                                                                                                                                                                                                                                                                           230 DHKFDEETTTNRDHFK 245
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Best Local Similarity 50.0%
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-361 < REA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: D81553
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A;Cross-references: UNIPROT:Q9KFY7; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB040 A;Experimental source: strain C-125 C;Genetics: A;Genet BH0329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-801 <STO>
A;Cross-references: UNIPROT:Q9KEZ5; GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB044
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T30251
R;Krieg, P.; Schuppler, M.; Koesters, R.; Mincheva, A.; Lichter, P.; Marks, F.
Genomics 43, 339-348, 1997
A;Title: Repetin (Rptn), a new member of the fused gene subgroup within the S100 gene fan
A;Reference number: Z20789; MUID:97422611; PMID:9268637
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A;Cross-references: UNIPROT:P97347; EMBL:X99251; NID:g1806131; PIDN:CAA67624.1; PID:g180
A;Experimental source: strain NMRI; clone 3031; skin papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: BH0704
C;Superfamily: lysosomal alpha-glucosidase; sucrase/isomaltase homology; trefoil homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glucosidase BH0704 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                       Length 423;
                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                       Score 42; DB 2;
Pred. No. 99;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: calcium binding; EF hand; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.5; DB 2
Pred. No. 3e+02;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DYKFY------EDANGTRDHK 17
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Search completed: November 24, 2004, 09:30:20 Job time : 16.6957 sec8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SDYKFYEDANGTRDHKK 18
                                                                                                                                                                                                                                                                                            38.3%;
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 2 - rape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 DYKFYENFN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DYKFYEDAN 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-269 < ROBS
A;Residues: 1-264 <GLA>
                                                                                                                      C;Genetica:
A;Gene: UU061
A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S51815
                                                                                                                                                                                                                                                                                            Query Match
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                                                             Signal peptidase (EC 3.4.99.-), microsomal - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: O7-Apr-1994 #sequence revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S22412; 840018; 51551
R;Newsome, A.L.; McLean, J.W.; Lively, M.O.
Biochem, J. 282, 447-4452, 1992
A;Title: Molecular cloning of a CDNA encoding the glycoprotein of hen oviduct microsomal A;Reference number: S22412; MUID:92189580; PMID:1546959
A;Title: Molecular cloning of a CDNA encoding the glycoprotein of hen oviduct microsomal A;Reference number: S22412; MUID:92189580; PMID:1546959
A;Accession: S22412
A;Molecule type: MRNA
A;Residues: 1-180 *NEM1>
A;Accession: S40018
A;Accession: S4018
A;Acces
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H69265
hypothetical protein AF0128 - Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Accession: H69265
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
C; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Wosee, C.R.; Venter, J.C.
A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Accession: H69265
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: L-202 < KLB>A;
A; Cross-references: UNIPROT:030109; GB:AE001097; GB:AE000782; NID:92689420; PIDN:AAB9110
C; Superfamily: conserved hypothetical protein AF1745
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Conserved hypothetical UU061 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G8233
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H. submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
A;Accession: G82339
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.3%; Score 41; DB 2; Length 180; Best Local Similarity 35.3%; Pred. No. 62; Matches 5; Indels Matches 5; Indels
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Best Local Similarity
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A;Cross-references: GB:AE002105; GB:AF222894; NID:g6899003; PIDN:AAF30466.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q39361; EMBL:L34288; NID:g2970638; PIDN:AAC06020.1; PID:g297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: S51815
R;Robert, L.S.; Allard, S.; Gerster, J.L.; Cass, L.; Simmonds, J.
Biol. 26, 1217-1222, 1994
A;Title: Molecular analysis of two Brassica napus genes expressed in the stigma. A;Reference number: S51814; MUID:95111105; PMID:7811980
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C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                               DB 2;
90;
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Best Local Similarity 41.2%; Pred. No. 91;
Matches 7; Conservative 4; Mismatches (
                                                                                                                                                               Score 41; DB 2
Pred. No. 90;
1; Mismatches
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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 142, Appli
Sequence 142, Appli
Sequence 142, Appli
Sequence 16870, Appli
Sequence 19901, Appli
Sequence 2599, Appli
Sequence 31901, Appli
Sequence 315, Appli
Sequence 3162, Appli
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Sequence 113, Appli
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Sequence 113, Appli
Sequence 113, Appli
Sequence 111, Appli
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                                                             November 24, 2004, 09:14:14; Search time 16.7283 Seconds (without alignments) 75.324 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
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US-08-841-089-2
US-09-841-089-2
US-09-301-085-2
PCT-US95-04570-2
US-08-310-912A-142
US-08-310-912A-142
US-09-310-085-142
US-09-248-796A-16970
US-09-248-796A-16970
US-09-248-796A-1458
US-09-248-796A-1458
US-09-134-078-2
US-09-134-078-2
US-09-134-078-2
US-09-134-010-3379
US-09-134-010-3379
US-09-134-010-3379
US-08-231-193A-11
US-08-486-273A-11
US-08-946-055A-11
US-08-946-035A-11
US-08-946-035A-11
US-08-948-77-11
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US-09-270-767-58231
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                  478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
                                                                                                                            1 RSDYKLYNKNSSTLKDLGE 19
                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                         Issued Patents AA:*
                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                     US-09-719-379A-4
98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                   Scoring table:
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43
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                                                                                                                                                                                                                            Minimum DB e
Maximum DB e
                                                                                                                              Sequence:
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Sequence Sequence

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Sequence 370, App
Sequence 1091, Ap
Sequence 6, Appli
Sequence 6, Appli
Sequence 1728, Ap
Sequence 911, Appli
Sequence 18781, Ap
Sequence 9, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskwicz, Brian J.
APPLICANT: Staskwicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Karagiri, Fundaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Kunkel, Barbara N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RFS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
TITLE OF INVENTION: METHODS
TITLE OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUMTRY: USA

ZIP: 02110-2904

COMPUTER READABLE FORM:
MEDTUM TYPE: FI-IDPDY disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/08/310,912A
FILING DATE: September 22, 1994
CLASSIFICATION NUMBER: 08/227,360
FILING DATE: April 13, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/254001
TELECOMMUNICATION NUMBER: 00786/254001
                 US-09-198-422A-1091

US-09-270-767-42905

US-09-404-258-6

US-09-853-701-6

US-09-853-701-6

US-09-853-701-91

US-09-198-422A-991

US-09-248-796A-18781

US-09-134-078-18

US-09-134-078-18

US-09-134-078-18

US-09-540-236-2373

US-08-66-167-4

US-08-06-177-2

US-08-06-167-4

US-08-06-167-4

US-08-06-197-6

US-08-06-197-6

US-08-06-197-6

US-08-08-198-2373

US-08-06-167-4

US-08-06-197-6

US-08-08-198-2373

US-08-08-198-2373

US-08-08-198-2373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERA.: (617) ...
TELERA: 100254
TELEX: 100254
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: amino acids
STRANDEDNESS: not relevant
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08310912A; Patent No. 5981730; GENERAL INFORMATION:
                   US-08-310-912A-2
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Patent No. 626248
GENERAL INFORMATION:
APPLICANT: Ataskawicz, Brian J.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Pumiaki
APPLICANT: Katagiri, Fumiaki
APPLICANT: Winkel, Barbara N.
APPLICANT: Winkel, B99-04-28
CURRENT FILING DATE: 1994-09-28
EARLIER APPLICATION NUMBER: 08/227,360
EARLIER FILING DATE: 1994-04-13
NUMBER OF SEQ ID NOS: 208
SOUTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH, 885
TAND: DATE: BARBARE SEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.0%; Score 49; DB 3; Length 885; Best Local Similarity 55.6%; Pred. No. 8.7; Matches 10; Conservative 3; Mismatches 5; Indels
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ZIP: 02110-5904

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
REDEADATE: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clast David The Parid 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Augubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Buniaki
APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Kunkel, Barbara N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9504570 GENERAL INFORMATION:
Sequence 2, Application US/09301085 Patent No. 6262248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 ADYKLCKKVSAILKSIGE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Clark, Paul T. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDALL
STREET: 220
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                                                                         DB 2; Length 885;
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                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
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ZIP: 02110-2904

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30B

CURRENT APPLICATION NUMBER: US/08/841,089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Augubel, Frederick M.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Pumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Kunkel, Barbara N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                         50.0%; Score 49; DB; 55.6%; Pred. No. 8.7;
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Pred. No. 8.7;
3; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
BPLICATION NUMBER:
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08841089
Patent No. 6127607
                                                                                                                                                                                                                                                                         103 ADÝKĽCKKVSAIĽKSIGE 120
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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55.6%;
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                                                       Query Match
Best Local Similarity 55.67
Matches 10; Conservative
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Best Local Similarity 55.6
Matches 10; Conservative
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MOLECULE TYPE: protein
US-08-841-089-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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STREET: 222
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      US-08-310-912A-2
                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-841-089-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-09-301-085-2
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Gaps

us-09-719-379a-4.rai

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A GENE FAWILY FROM THE 12 FUSARIUM RESISTANCE
LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
SELECTIVE BREEDING OF TOMATO AND RELATED FLANTS
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Length 885;
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                                                                                           Indels
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COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,996A
FILING DATE: 09-DEC-1997
PRIOR APPLICATION NUMBER: PCT/US96/05272
FRING DATE: 15-APR-1996
PRIOR APPLICATION NUMBER: IL 113,373
APPLICATION NUMBER: IL 113,373
INFORMATION PCR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENDTH: 907 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ORI, Maconi
APPLICANT: ORI, Maconi
APPLICANT: PARAN, Ilan
APPLICANT: ZAMIR, Daniel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FT
TITLE OF INVENTION: SELECTIVE BREEDING OF TOWATC
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: BROWDY AND NSIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
         Score 49; DB 9
Pred. No. 8.7;
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Best Local Similarity 55.6%; Pred. No. 8.9;
Matches 10; Conservative 3; Mismatches
                                                                                           3; Mismatches
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; Sequence 142, Application US/08310912A
; GENERAL INFORMATION:
    APPLICANT: Staskawicz, Brian J.
    APPLICANT: Brent, Andrew F.
    APPLICANT: Brent, Andrew F.
    APPLICANT: Brent, Andrew F.
    APPLICANT: Katagiri, Pumiaki
    APPLICANT: Kunkel, Barbara N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08930996A
Patent No. 6100449
                                                                                                                                                                                                                                                                    103 ADÝKĽCKKVSAIĽKSIĠE 120
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111 ADYKLCKKVSAILKSIGE 128
                                                                                                                                                                                  2 SDYKLYNKNSSTLKDLGE 19
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Query Match 50.0%;
Best Local Similarity 55.6%;
Matches 10; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLUHR, Robert
ESHED, Yuval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-930-996A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: PCT/US95/04589

PILING DATE:
CLASSIFICATION NUMBER: PCT/US95/04589

FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
TELERAX: (617) 542-8906
TELERAX: (617) 542-8906
TELERAX: 100254
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRAACTERISTICS:
LENGTH: 885 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Dablbeck, Douglas
APPLICANT: Karagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindrinos, Michael N.
APPLICANT: Windrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSER: Rish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49; DB :
Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUTCATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 Franklin Street Suite
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2904
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9504589 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|||| | |: || :||
103 ADYKLCKKVSAILKSIGE 120
                                                                                                                           TELEFAX: (617) 542-8906
TELEFAX: 100294
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 amino acids
TYPE: Amino acids

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STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.6
Marches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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Gaps

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5; Indels

3; Mismatches

Score 49; DB 3; Length 909;

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2 SDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                TYPE: PRT; ORGANISM: Arabidopsis thaliana
US-09-301-085-142
                                                                                                                                                                                                                                                                          Cuery Match
Best Local Similarity 55.6%;
Matches 10; Conservative
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                                                                                                               SEQ ID NO 142
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APPLICANT: Mindrinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Pi-'
STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sequence 142, Application US/09301085

; Patent No. 626248

; Patent No. 626248

; Patent No. 626248

; APPLICANT: Ausubel, Frederick M.

APPLICANT: Brent, Andrew F.

APPLICANT: Katagiri, Fumiaki

APPLICANT: Katagiri, Fumiaki

APPLICANT: Winkel, Barbara N.

APPLICANT: Windrinos, Michael N.

APPLICANTON NUMBER: US/09/301,085

CURRENT FILING DATE: 1999-04-28

EARLIER FILING DATE: 1994-09-22

; EARLIER FILING DATE: 1994-09-22

; BARLIER FILING DATE: 1994-04-13

; NUMBER OF SEQ ID NOS: 208

; NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 02110-2904

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310,912A

FILING DATE: September 22, 1994

CLASSIFICATION S54

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/227,360

FILING DATE: April 13, 1994

ATOONEY/AGBAT INPORMATION:

REGISTRATION NUMBER: 35,238

REGISTRATION NUMBER: 35,238

RESTRENCE/POCKET NUMBER: 35,238

REGISTRATION NUMBER: 35,238

RESTRENCE/POCKET NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 49; DB
Pred. No. 8.9;
3; Mismatches
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111 ADYKLCKKVSAILKSIGE 128
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INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 909 amino acids
TYPE: amino acid
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Best Local Similarity 55.6%;
Matches 10; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                      Boston
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                                                                                                                                                                                                                                                                                                                                         CITY: BOB!
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589
FILING DATE:
CLASSIFICATION STA:
PRIOR APPLICATION NUMBER: US 08/227,360
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
AND STATEMENT OF THE S
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ausubel, Frederick M.
APPLICANT: Ausubel, Frederick M.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Fumiaki
APPLICANT: Kankel, Barbara N.
APPLICANT: Kunkel, Barbara N.
APPLICANT: Mindtinos, Michael N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201
CORRESPONDENCE ADDRESS:
ADDRESSEB: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Clark, Paul T.
REGISTRATION VNDRER: 30,162
REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                PCT-US95-04589-142; Sequence 142, Application PC/TUS9504589; GENERAL INFORMATION:
111 ADYKLCKKVSAILKSIGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||| | |: || :||
111 ADYKLCKKVSAILKSIGE 128
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INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 SDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 542-5070
(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 909 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) MOLECULE TYPE: protein
PCT-US95-04589-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                         US-09-134-078-21
| Sequence 21, Application US/09134078
| Patent No. 636844
| GENERAL INFORMATION:
| APPLICANT: Bylina, Edward J.
| TITLE OF INVENTION: GLYCOSIDASE ENZYMES
| NUMBER OF SEQUENCES: 72
| CORRESPONDENCE ADDRESS:
| ADDRESSES: Gray Cary Ware & Freidenrich LLP |
| STREET: 4365 Executive Drive, Suite 1600
| CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACTION
OPERATING SYSTEM: Windows95
SOFTWARE: FASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-AUG-1998
CLASSIFCATION NATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 06/056,916
FILING DATE: 06-DEC-1996
FILING DATE: 06-DEC-1996
FILING DATE: 06-DEC-1996
FILING DATE: NEORMATION:
                                                                                                                                                                 4
                                                                                                                                                                                 Pred. No. 84;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REPERENCE/DOCKET NUMBER: 09010/024002
TELECOMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 14458, Application US/09248796A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                            Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                559 KYYNINQTVMKDLSE 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                       5 KLYNKNSSTLKDLGE 19
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58 NSYELYERDQEIAKDLG
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19901
LENGTH. 820
TYPE: PRT
                                                                                      ; ORGANISM: Candida albicans
US-09-248-796A-19901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
internal
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FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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                                 Sequence 16870, Application US/09248796A
Patent No. 6747137
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196-113
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR PLILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19901, Application US/09248796A

Patent No. 6747137

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: WHBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORDATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO S: 5599
LENGTH: 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.4%; Score 44.5;
llarity 45.5%; Pred. No. 41
Conservative 5; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45;
Pred. No.
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Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSDYKLYNKNSST----LKDL 17
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-5599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RSDYKLYNKNSSTLKDLG 18
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78 RDDYEFMIANPLIMKDLG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.9%;
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; ORGANISM: Candida albicans
US-09-248-796A-16870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 9; Conservative
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nes 10; Conserve
                          US-09-248-796A-16870
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Best Local S
Matches 10
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US-08-231-193A-11

Sequence 11, Application US/08231193A

Patent No. 549895

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie P.

APPLICANT: Liaw, Chen W.

APPLICANT: Lu, Chin-Chun

TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR

TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSES:

ADDRESSES:

CITY: San Diego

CITY: San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 153, Application US/09809665A; Sequence 153, Application US/09809665A; Batent No. 6790950; GENERAL INFORMATION:
APPLICANT: LOWERY E., David, et al.
APPLICANT: LOWERY E., David, et al.
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions; PILE REFERENCE: 28341/00435 US/09/809,665A; CURRENT APPLICATION NUMBER: 60/153,453 PRIOR PILING DATE: 1999-09-10
PRIOR PLILING DATE: 1999-04-09; PRIOR APPLICATION NUMBER: 60/128,689
PRIOR PLILING DATE: 1999-04-09; PRIOR PLILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                          Query Match
42.3%; Score 41.5; D
Best Local Similarity 37.5%; Pred. No. 57;
Matches 9; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.3%; Score 41.5; I ilarity 55.6%; Pred. No. 59; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Actinobacillus pleuropneumoniae
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER 0F SEQ ID NOS: 5674
SEQ ID NO 3379
LENGTH: 357
TYPE: PRT
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3379
                                                                                                                                                                                                                                                                                                                                                                       316 RNDYRFYPSNQEQQRLEVYKDLGQ 339
                                                                                                                                                                                                                                                                                                                          1 RSDYKLYNKNS----STLKDLGE 19
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IBM PC compatible
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COMPUTER READABLE FORM:
MEDIJIM TYPE: Floppy d3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10, Conserv
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                         GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

SEQ ID NO 14458

LENGTH: 591
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TILLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3262
LENGTH: 176
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84;
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Patent No. 6380370
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Patent No. 6703492
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ORGANISM: Artificial Sequence
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442 DYQLFQKTNQNFKDL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14458
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nes 9; Conserva
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1184 YKLYSKH-FTLKDKG 1197
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1184 YKLYSKH-FTLKDKG 1197
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 amino acids
TYPE: âmino acid
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LENGTH: 1464 amino acids
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Best Local Similarity 66.7
Matches 10; Conservative
                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-940-086A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                      US-08-486-273A-11
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US-08-486-273A-11
US-08-486-273A-11
Sequence 11, Application US/08486273A
Facett No. 5985586
GENERAL INFORMATION:
APPLICANT: Daggett, Lorrie P.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTRO SUBUNITS, DNA
TITLE OF INVENTION: ENCODING SAME AND USES THEREFOR
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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              SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: US/08/231,193A
FILING DATE: 20-APR-1994
CLASSIFICATION: 536
PRICE APPLICATION TAN:
APPLICATION NUMBER: US 08/052,459
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie
REFERENCE/DOCKET NUMBER: 6362-9383
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER TO S. A.

ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUW TYPE: FIDOPY disk
COMPUTER: IBM PC Compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,273A
PILING APPLICATION: 435
PRIOR APPLICATION HOMBER: US/08/486,273A
PILING APPLICATION: 435
PRIOR APPLICATION WHERE: US/08/231,193
FILING DATE: 20-APR-1994
CLASSIFICATION: 435
ATONNEY/AGENT INFORMATION:
NAME: Setdman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/POCKET NUMBER: 6362-9383B
TELEPHONE: 619-238-0999
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1184 YKLYSKH-FTLKDKG 1197
                                                                                                                                                                                                                                                                                                                                                                                    1464 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 YKLYNKNSSTLKDLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           619-238-0062
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Supplication acida

Supplication acida

TOPOLOCOY: linear

TOPOLOCOY:
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RESULT 23
US-08-935-105A-11
Sequence 11, Application US/08935105A
Sequence 11, Application US/08935105A
Sequence 11, Application US/08935105A
APPLICANT: Daggett, Lorrie P.
APPLICANT: Lu, Chin-Chun
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41.5; DB 3; Length 1464;
Pred. No. 30+02;
2; Mismatches 2; Indels 1;
COMPUTE: 72.037

COMPUTE: FLADABLE FORM:
MEDIUM TYPE: FLODPY disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,035A
FILING DATE: 29-SEPT-97
PRIOR APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
CLASSIFICATION: 536
ATTONREY/AGENT INPORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 31,779
REGISTRATION NUMBER: G19-238-0999
TELEEPAK: 619-238-0099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,105A
FILING DATE: 29-SEPT-97
PRIOR APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1994
CLING DATE: 20-APR-1993
CLASSIFICATION: 536
CLASSIFICATION: 536
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TYPE: IBM PC compatible
TYPE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1464 amino acida
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YKLYNKNSSTLKDLG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-940-035A-11
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Sequence 11, Application US/08940035A

PARENT INFORMATION:

APPLICANT: Diagrat, Lorrie P.

APPLICANT: Liaw, Chen W.

APPLICANT: Liaw, Chen W.

TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR TITLE OF EXQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McAuliffe

STREET: 4250 Executive Square, 7th Floor

CITY: La Jolla
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                                                                                                                      Sequence 10, Application US/08436332B
Patent No. 6130058
GENERAL INFORMATION:
APPLICANT: LE BOUNDELLES, BEATRICE
APPLICANT: WHITING, PAUL JOHN
TITLE OF INVENTION: STABLY TRANSFECTED CELL LINE EXPRESSING
TITLE OF INVENTION: RECEPTORS, AND NOVEL CLONED NMDA
TITLE OF INVENTION: RECEPTOR SUBUNIT SEQUENCES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: MICHAEL D. YABLONSKY - MERCK & CO., INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: MICHAEL D. YABLONSKY - MERCK & CO., INC.
126 EAST LINCOLN AVE., - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,332B

FILING DATE: 10-MAY-1995

CLASSITCATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: YABLONSKY, MICHAEL D.

REGISTRATION NUMBER: 40,407

REFERENCE/DOCKET NUMBER: 71210Y

TELEPHONE: 732-594-4778

TELEPHONE: 732-594-4778

INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:

LENGTH: 1464 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 126 EAST LI
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065
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                                                   RESULT 21
US-08-436-332B-10
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US-08-940-035A-11
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Query Match 42.3%; Score 41.5; DB 4; Length 1464; Best Local Similarity 66.7%; Pred. No. 3e+02; Matches 10; Conservative 2; Mismatches 2; Indels 1;
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MEDIUM TYPER: RIOPPY disk

MEDIUM TYPER: RIOPPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/217,704C

FILING DATE: 25-Mar-1994

PRIJIG DATE: 12-DEC-94

ATTORNEY/AGENT INFORMATION:

NAME: Benc, Stephen A:

REGISTRATION NUMBER: 29.768

REGISTRATION NUMBER: 29.768

REFERENCE/DOCKET NUMBER: 16717/259/ALLE

TELECOMMUNICATION NUMBER: 16717/259/ALLE

TELERHONE: (202), 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Foldes, Robert
Fantaske, Robert
Adams, Sally-Lyn
Kamboj, Rajender
TITLE OF INVENTION: MODULATORY PROTEINS OF HUMAN CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLGY & Lardner
STREET: Suite 500, 3000 K Street
CITY: Washington, D.C., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-08-217-704C-2
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08217704C; Patent No. 6489124; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09386123; Patent No. 6521413; GENERAL INFORMATION: APPLICANT: Daggett, Lorrie P. APPLICANT: Ellie, Steven B. APPLICANT: Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 672-5399
                                                                                                                                                                                          1184 YKLYSKH-FTLKDKG 1197
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Matches 10; Conservative
                                                                                                                                               4 YKLYNKNSSTLKDLG
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                            US-08-217-704C-2
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US-09-386-123-11
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LU, CHINDAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/940,086A
FILING DATE: 29-SEPT-97
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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CORRESPONDENCE HADDRESSE: HADDRESSE: HADDRESSE: HADDRESSEE: HADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9383C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.3%; Score 41.5; D
Best Local Similarity 66.7%; Pred. No. 3e+0
Matches 10; Conservative 2; Mismatches
                 REPERENCE/DOCKET NUMBER: 33,779
REPERENCE/DOCKET NUMBER: 6362-9383D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-099
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1464 amino acids
TYPE: amino acids
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1 MOLECULE TYPE: protein
2 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-648-797-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 450-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09648797
Patent No. 6469142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Daggett, Lorrie P.
Ellis, Steven B.
Liaw, Chen W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1464 amino acids
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       Seidman, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 YKLYNKNSSTLKDLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-935-105A-11
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Gaps

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Indels

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64.3%; Pred. No. 20; tive 2; Mismatches

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9; Conservative
Best Local Similarity
Matches 9; Conserva
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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    HUMAN N-METHYL-D-ASPARTATE RECEPTOR
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
63
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Patent No. 6703491.

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58231
LENGTH: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.3%; Score 41.5; DB 4; Length 1464; 66.7%; Pred. No. 3e+02; Live 2; Mismatches 2; Indels 1;
                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 92037

COUNTER READBALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/386,123

FILING DATE:
TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTAT
TITLE OF INVENTION: SUBUNITS, NUCLEIC ACIDS E
NUMBER OF SEQUENCES: 63
CAPRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
SIREET: 4250 Executive Square, 7th Floor
CITY: La Jolla
SIATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58231
                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE:

APPLICATION DATA:
APPLICATION UNMBER: 08/486,273
FILING DATE: 06-JUNE-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,193
FILING DATE: 20-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,449
FILING DATE: 20-APR-1993
CLASSIFICATION:
ATTONEY, AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6562-9383F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-567-5360
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTER/STICS:
STOWMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1184 YKLYSKH-FTLKDKG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 YKLYNKNSSTLKDLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 66.7
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear; MOLECULE TYPE: protein US-09-386-123-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 27
US-09-270-767-58231
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41.8%; Score 41; DB 4; Length 126;

Query Match

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Sequence 1091, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: Inference and uses thereof, in particular for the diagnosis, preverence of the properties of 10-003-999
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION WINBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Holland, Ross
APPLICANT: Feid, Julian R.
APPLICANT: Cololear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them and methods for using them.
FILE REFERENCE: 11000.104101/01/02/034,238
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.8%; Score 41; DB 4; nilarity 44.4%; Pred. No. 31; Conservative 2; Mismatches 8
                                                                                                                                                     US-09-634-238-370
; Sequence 370, Application US/09634238
Patent No. 6544772
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                     Glenn, Matthew
Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
Christensson, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 SDYQAINPTFGTMKDFDE 127
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; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1091
                          || |: |:|||||
79 KLKNEMMSSLKDLG 92
5 KLYNKNSSTLKDLG 18
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 9; Conserv
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    Sequence 42905, Application US/09270767

Sequence 42905, Application US/09270767

Sequence No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 42905

LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09404258

Patent No. 6274353

GENERAL INFORMATION:
APPLICANT: YANG, Shuwei

TITLE OF INVENTION: SYNTHESIS
FILE REFERENCE: 089952/0102

CURRENT PILLING DATE: 1999-09-22

NUMBER OF SEQ ID NOS: 17
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GENERAL INFORMATION:
APPLICANT: YANG, Shuwei
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR IMPROVED POLYNUCLEOTIDE
TITLE OF INVENTION: STWITHESIS
FILE REFERENCE: 089962/0102
CURRENT PILING DATE: 2001-05-14
PRIOR PLILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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61.5%; Pred. No. 52;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                       4; Length 273;
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                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Xaa means any amino acid US-09-270-767-42905
                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09853701
Patent No. 6699981
                                                                                                                                                                                                                                                                                                                                                                                     41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Pyrococcus furiosus
US-09-404-258-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 KLKNEMMSSLKDLG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S KLYNKNSSTLKDLG 18
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Best Local Similarity 64.3-
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Matches 8; Conservative
US-09-270-767-42905
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Sequence 4728, Application US/09543681A
Sequence 4728, Application US/09543681A
Bateint No. 6655709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                 RESULT 33
US-08-210-394-1
Sequence 1, Application US/08210394
Sequence 1, TITLE OF INVENTION: Purified No. 5770213typable
TITLE OF INVENTION: Influence P5 Protein as a Vaccine for No. 5770213typable
TITLE OF INVENTION: Haemophilus Influence Strain
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                      Score 41; DB 4; Length 281;
Pred. No. 52;
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65;
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210,394
FILING DATE: 07-MAR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.8%; Score 41; DB ilarity 61.5%; Pred. No. 65; Conservative 1; Mismatches
                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALUNESSEE: American Cyanamid Company STREET: One Cyanamid Plaza CITY: Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORTATION:
NAME: Harrington, James J
REFERENCE/DOCKET NUMBER: 32,3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201/831-3246
TELEPAX: 201/831-3305
                                                                                        41.8%;
61.5%;
TYPE: PRT : ORGANISM: Pyrococcus furiosus US-09-853-701-6 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201/831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                          119 RSDYKFYEAPNST 131
                                                                                                                                                                               5 KLYNKNSSTLKDL 17
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                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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                                                                                                               Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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US-09-543-681A-4728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-210-394-1
                                                                                           Query Match
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APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Madahl, Lars G.
APPLICANT: Chen, Huizhong
APPLICANT: Chen, Huizhong
TITLE OF INVENTION: Beta-glucosidase Coding Sequences and Protein from
TITLE OF INVENTION: Orpinomyces PC-2
TITLE OF INVENTION: DATE: 1999-05-06
FILE REPERENCE: 31-98us
CURRENT FILING DATE: 1999-05-06
BARLIER PRILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver: 2.0
SEQ ID NOS: 13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTEN: Mindows95
SOFTWARE: FASTEN: Mindows95
SOFTWARE: A35
PRIOR APPLICATION NUMBER: 08/949,026
FILING DATE: 10-0CT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: MOREN: 60-056,916
FILING DATE: Mindowation:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: A38,347
PREGISTRATION NUMBER: Manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600 CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09134078
; Batent No. 6368844
; GENERAL INFORMATION:
    APPLICANT: Bylina, Edward J.
    TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; TUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 09010/024002 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                 Sequence 9, Application US/09306593
Patent No. 6184018
GENERAL INFORMATION:
                                                        339 KSEYQSLEKCSSTIKD 354
                            1 RSDYKLYNKNSSTLKD 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 YKKYKEDVKLLKDLG 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Costus speciosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                             US-09-306-593-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 476
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FLING DATE: 1998-02-13
PRIOR FLING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 991
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                                                                                                                                                                                                                                                                         Score 41; DB 4; Length 342;
Pred. No. 66;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 41.8%; Score 41; DB 4; Length 351; Best Local Similarity 61.5%; Pred. No. 68; Matches 8; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.8%; Score 41; DB 4; Length 388;
50.0%; Pred. No. 76;
iive 4; Mismatches 4; Indels
CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 SEQ ID NO 4728 LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18781, Application US/09248796A
Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 991, Application US/09198452A Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     :::||| | ||:|
126 RIHNKNPSIEKDIG 139
                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4728
                                                                                                                                                                                                                                                                                                                                                                            5 KLYNKNSSTLKDLG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 KLYNQSKTTGKDL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18781
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S KLYNKNSSTLKDL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-248-796A-18781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-198-452A-991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Xaa' at location 294 stands for Thr, Ala, Pro, or Ser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (235)..(235)
OTHER INFORMATION: The 'Xaa' at location 235 stands for Glu, Asp, or Ala.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEX: misc feature
LOCATION: (215)..(215)
OTHER INFORMATION: The 'Xaa' at location 215 stands for Glu, or Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (236)..(236)
OTHER INFORMATION: The 'Xaa' at location 236 stands for Lys, or Asn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHORT, Jay M.

TITLE OF INVENTION: DIRECTED EVOLUTION OF THERMOPHILIC ENZYMES
FILE REFERENCE: 112766-222(DIV-1460-22)
CURRENT APPLICATION NUMBER: US/10/039,293A
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: US 09/185,373
PRIOR PRILING DATE: 1998-11-03
PRIOR PILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: US 08/760,489
PRIOR FILING DATE: 1996-12-05
PRIOR FILING DATE: 1995-12-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Version 3.1
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LOCATION: (224)..(224)
OTHER INFORMATION: The 'Xaa' at location 224 stands for Gly
                                                                                                                                                                                                                                                  41.8%; Score 41; DB 3; Length 509 41.2%; Pred No. 1e+02;
                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Thermococcus 9N2 Beta-glycosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10039293A
Patent No. 6713281
              TELERAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 509 amino acide TYPE: amino acid TOPOLOX: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                             2 SDYKLYNKNSSTLKDLG 18
                                                                                                                                                                                                                                                                                                                                                                          ::|:|| |: :||| |: 58 NNYELYEKDHRLARDLG 74
858/677-1456
                                                                                                                                                                                                                               Query Match
Best Local Similarity 41.23
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (281)...(281)
OTHER INFORMATION: The
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LOCATION: (284)..(284)
OTHER INFORMATION: The
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LOCATION: (294)...(294)
OTHER INFORMATION: The
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LOCATION: (295)..(295)
TELEPHONE:
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US-09-134-078-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 39
US-10-039-293A-2
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Sequence 2373, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT PELING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
ENGINE OF 2373
ENGINE OF 2373
or Ser.
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OTHER INFORMATION: The 'Xaa' at location 295 stands for Thr, Ala, Pro,
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                                                                Length 509
                                                                                                        5; Indela
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Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 4.
                                                              Score 41; DB 4;
Pred. No. 1e+02;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 24, 2004, 09:31:41
Job time : 17.7283 secs
                                                                                                                                                2 SDYKLYNKNSSTLKDLG 18
                                                                                                                                                                          58 NNYELYEKDHRLARDLG 74
                                                  Query Match 41.8%;
Best Local Similarity 41.2%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| :| |||||||
467 ELVKQNHGTLKDLGK 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 KLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
, ORGANISM: M.catarrhalis
US-09-540-236-2373
                                                                                                                                                                                                                                                                              US-09-540-236-2373
        US-10-039-293A-2
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November 24, 2004, 09:11:04; Search time 87.3587 Seconds (without alignments) 125.141 Million cell updates/sec Run on:

US-09-719-379A-4 98 1 RSDYKLYNKNSSTLKDLGE 19 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		d			SUMMAKIES	
Result		Query				
No.	Score	Match	Match Length	DB	di.	Description
-	87	88.8	353	-	OMS1 HAEIN	
8	19	62.2	907	N	Q8LL02	
e	20	51.0	289	~	Q8ZV60	
4	20	51.0	1043	N	Q7RLC4	
Ŋ	49	20.0	167	ч	RPO7 FOWPV	Q05569 fowlpox vir
9	49	20.0	167	N	Q70G <u>Z</u> 1	Q70gzl fowlpox vir
7	49	20.0	167	N	CAE52706	Cae52706 fowlpox v
80	49	20.0	179	N	Q7ZUH7	Q7zuh7 brachydanio
6	49	20.0	606	Н	RPS2 ARATH	Q42484 arabidopsis
10	49	50.0	606	N	AA064907	0
11	48	49.0	394	N	оэотнэ	
12	48	49.0	430	N	Q9YVTS	
13	48	49.0	450	N	Q6HM95	
14	48	49.0	450	N	Q73C96	Q73c96 bacillus ce
15	48	49.0	450	N	Q81U20	Q81u20 bacillus an
16	48	49.0	450	N	AAS40100	Aas40100 bacillus
17	48	49.0	450	~	AAT30173	
18	48	49.0	505	Н	SPKD SYNY3	P54735 synechocyst
19	48	49.0	549	N	Q81K31	Q81k31 bacillus an
20	48	49.0	549	~	AAT34652	Aat34652 bacillus
21	48	49.0	802	N	Q9QP04	Q9qp04 human immun
22	48	49.0	851	~	Q9QBY6	Q9qby6 human immun
23	47	48.0	181	~	Q9V832	Q9v832 drosophila
24	47	48.0	294	~	Q72WS2	Q7zws2 xenopus lae
25	47	48.0	720	~	Q7MV25	Q7mv25 porphyromon
56	46	46.9	268	~	Q6LX25	Q61x25 methanococc
27	46	46.9	268	~	CAF31084	Caf31084 methanoco
28	46	46.9	450	7	Q81GW3	Q81gw3 bacillus ce
29	46	46.9	465	~	Q9PJ81	
30	46	46.9	530	~	Q8X0E9	
31	46	46.9	784	N	Q8BJQ2	Q8bjq2 mus musculu

Q8vel7 mus musculu Q8vem4 mus musculu Q8vem4 mus musculu Q33845 thermococcu Q7X545 plasmodium Aaq73468 plasmodium Q8hpj plasmodium Q8thpj plasmodium Q8t5c7 plasmodium Q6tb6 kluyveromyc	Q61205 picrophilus Q72sx1 leptospira Q8f2k3 leptospira Aas69857 leptospir
Q8VE17 Q8VEM4 DPOL THEST DPOL AAQ73469 Q7KSQ5 AAQ73468 AAQ73468 Q8TEQ7 Q6CJB6	Q6L205 Q72SX1 Q8F2K3 AAS69857
00000000000000000000000000000000000000	0000
784 1829 2006 2006 2019 2019 2055 4915	320 60 60
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4.0.0.0 4.0.0.0
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	45.5 45 45 45 5
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ALIGNMENTS

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Gaps

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Length 289; 3; Indels

CHAIN

WI THE SO

Best Loca Matches

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"Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Koeack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Prorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                      "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                   Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary derived the EMBL; AABLO1000722; EAA22094.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
NON TER 1043 1043
SEQUENCE 1043 AA; 122316 MW; OCE7D5C185132E2E CRC64;
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                          289 AA; 30809 MW; 4914994B4FD110C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002)
EMBL; AB009876; AAL64196.1; -.
InterPro; IPR003462; ODC_Mu_crystall.
Pfam; PP07423; OCD_Mu_crystall; 1.
COMPlete protecme.
SEQUENCE 289 AA; 30809 MW; 4914994B4FD110r6
                                                                                                                                                                                                                                                                                                                                         51.0%; Score 50; DB 2;
50.0%; Pred. No. 20;
tive 5; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 2;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1043 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                          SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:||:||:
141 YKIYNRDSKKAEDLGK 156
                                                                                                                                                                                                                                                                                                                                                                                                                        4 YKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.0%;
55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12368865;
                                                                                                                                                                                          aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carucci D.J.;
                                                                                                                                                         Miller J.H.;
                                                                                                                                                                                                                                                                                                                                             Query Match
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Rps2 of Arabidopsis thallana.";

Rps2 of Arabidopsis thallana.";

Genetics 163:735-746(2003).

EMBL; AF487796; AAM90888.1; -.

GO; GO:00005524; F:ATP binding; IEA.

GO; GO:00006915; P:apoptosis; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006915; P:apoptosis; IEA.

R GO; GO:0006915; P:apoptosis response to pathogen; IEA.

R InterPro; IPR00157; Disase_resist.

R InterPro; IPR001611; IRR.

R InterPro; IPR001181; IRR.

R PF00911; NB-ARC.

R Pfam; PF00931; NB-ARC; 1.
                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis lyrata (Lyre-leaved rock-cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
 Complete protecome, Outer membrane, Porin, Signal, Transmembrane.
SIGNAL 1 21 By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                   88.8%; Score 87; DB 1; Length 353; llarity 89.5%; Pred. No. 3.9e-05; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.2%; Score 61; DB 2; Length 907; 66.7%; Pred. No. 1.3; ive 3; Mismatches 3; Indels
                   By similarity.
Outer membrane protein P5.
By similarity.
OmpA-1ike.
W; 64ACB3E7BFP96B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22505406; PubMed=12618410;
Mauricio R., Stahl E.A., Korves T., Tian D., Kreitman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907 AA; 104220 MW; EE3147059171FCC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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(TrEMBLrel. 20, Last sequ
(TrEMBLrel. 26, Last anno
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OrderedLocusNames=PAE2445;
Pyrobaculum aerophilum.
                                                                                                                                                                                                                                                 132 RSDYKLYNENSSTLKKLGE 150
                                                                                                                                                                                                               1 RSDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||| || |:||| :||
111 ADYKLCNKVSATLKSIGE 128
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338 By
316 Om
37743 MW;
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Best Local Similarity 66.7%,
--hes 12; Conservative
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ATP-binding.
                                       22 3
326 3
272 3
353 AA;
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                                                                                                                                                       Local Similarity
tes 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=59689;
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01-OCT-2002 (
01-MAR-2004 (
RPS2.
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01-MAR-2002 (
01-MAR-2004 (
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SEQUENCE
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08ZV60;
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Q8LL02;
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RESULT 3 Q8ZV60 ID Q8ZV AC 01-EV DT 01-M DT 01-M DT 01-M GN Orde OS PYFO

ઠે g Length 1043;

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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                            ASR RPO19 orthologue.
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                                                                                                                                                          NCBI_TaxID=10263;
                                                                                                                                    Avipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RNA)(N).
SUBUNIT: This enzyme consists of at least eight subunits.
                                      50.0%; Score 49; DB 1; Length 167; 38.9%; Pred. No. 17; ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-directed RNA polymerase; Early protein; Transcription;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=90209363; PubMed=2157318;
Kumar S., Boyle D.B.;
"Mapping of a major early/late gene of fowlpox virus.";
virus Res. 15:175-186(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 AA; 19500 MW; D67E10A724179C37 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X52461; CAA36694.1; -.
EMBL; AF198100; AAF44513.1; -.
EMBL; AJ005164; CAA06407.1; -.
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16 NDYKSYDEDDDSISDIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-97 FROM N.A
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Matches 7; Conservative
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                                                                                                                                                                              Fowlpox virus (FPV).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                  Avipoxvirus.
NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substrates.
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Q70GZ1;
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Avipoxvirus; Fowlpox virus.
NCBI_TaxID=10263;
                                                                                                                                              Viruses, dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Skinner M.A., Laidlaw S.M.;
Skinner M.A., Laidlaw S.M.;
Skinner B.A., Laidlaw S.M.;
American and European fowlpox virus, with those of virulent American and European viruses.";
J. Gen. Virol. 88:1305-222 (2004).

EMBL; AJ581527; CAR52706.1;
InterPro; IPR007984; Pox RNA Pol 19.
Pram; PP05220; Pox RNA Pol 19;
Predom; PD012915; Pox RNA Pol 19; 1.
ProDom; PD012915; Pox RNA Pol 19; 1.
SEQUENCE 167 AA; 19500 MW; D67B10A724179C37 CRC64;
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Skinner M.A., Laidlaw S.M.;
Comparison of the genome sequence of FP9, an attenuated, tissue
culture-adapted Buropean fowlpox virus, with those of virulent
American and European viruses.";
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AXS81527; CAES2706.1;
Serine processe inhibitor.
SEQUENCE 167 AA; 19500 WW; D67E10A724179C37 CRC64;
Created)
Last sequence update)
Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 49; DB 2; 38.9%; Pred. No. 17; ive 7; Mismatches 4
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                                                                                                                           Fowlpox virus (isolate HP-438[Munich]).
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27,
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Matches 7; Conservative
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Matches 7; Conservative
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Straubberg R.L., Feingeld E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soarse M.B., Bonaldow M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan K.J., Mazke J.A., Guazarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
And Marra M.J., Schmutz J., Myers R.W., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Add. Mones S.J., Marra M.A.,
Shalak B. M. Schnerch A., Schein J.E.,
Schnerztion and initial analysis of more than 15,000 full-length human
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PRT; 909 AA.
Q42464; O82096; O8L3W3; Q8L4X9; Q8L4Y0; Q8L587; Q8L5B3;
Q8LKZ8; Q8LL00; Q9LL00; Q9ASP5;
Q0LCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 44, Last annocation update)
10-OCT-2004 (Rel. 44, Last annocation update)
10-OCT-2005 (Rel. 44, Last sequence update)
10-OCT-2005 (Rel. 44, Last sequence update)
10-OCT-2007 (Rel. 44, Last sequence update)
10-OCT-2008 (Rel. 44, Last sequence update)
10-OCT-2009 (Rel. 42, Last sequence update)
10-OCT-2009 (Rel. 44, Last sequence update)
10-OCT-2009 (Rel. 42, Last sequence updat
                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC049039; AAH49039.1; -.
GO; GO:0003723; F:RNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEGUENCE 179 AA; 20996 MW; 9960F6A2EB5BA3AF CRC64;
                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein zgc:56526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
   179 AA.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Whole body;
MEDLINE=22388257; PubMed=12477932;
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Pfam; PP01479; S4; 1.
SMART; SM00363; S4; 1.
PROSITE; PS50889; S4; 1.
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   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7955;
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RC STRAINE-CV. Columbia;

RC STRAINE-CV. Columbia;

REACHERE CON MANDULT R., Murphy G., Volckaert G.,

RA MAPER K.F.X., Schueller C., Wambutt R., Butian K.-D., Terryn N.,

RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

RA Pohl T., Duesterhoeft B., Stiekema W., Entian K.-D., Terryn N.,

RA Pohl T., Duesterhoeft B., Stiekena W., Schuidthein T.,

RA Weichselgartner W., Puigdomenech P., Watson M., Schmidthein T.,

RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidthein T.,

RA Von P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,

Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Langham S.-A., McCullagh B., Bilham L., Robben J.,

RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,

RA Bracken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defcor E.,

RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

RA Molfaer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,

RA Berneiser S., Hempel S., Feldpaucch M., Villarroel R., De Clercq R.,

RA Der Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,

RA Monifaen P., Rlein Lankhorst R., Rose M., Hauf J., Rochnert S.,

RA Mondiewan M., Fartmann B., Granderath K., Dauner D., Herzl A.,

RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Massenet O., Quigley F., Clabauld G., Muendlein A., Pelber R.,

RA Achnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,

Chefdor F., Cooke R., Berger C., Monfort A., Caron D., Josse T.,

RA Peter-Perez A., Purnelle B., Bent B., Johnson S., Francs P., Bielke C.,

RA Peter-Perez A., Purnelle R., Bent B., Johnson S., Francs P., Bielke C.,
                                                                                                                                                                                                                                                                    STRAIN=cv. Columbia;
MEDLINE=94377978; PubMed=8091210;
Bent A.F.; Kunkel B.N., Dahlbeck D., Brown K.L., Schmidt R.,
Giraudat J., Leung J., Staskawicz B.J.;
"RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banerjee D., Zhang X., Bent A.F.; "The leucine-rich repeat domain can determine effective interaction between RPS2 and other host factors in Arabidopsis RPS2-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Natural selection for polymorphism in the disease resistance gene rps of Arabidopsis thaliana.";
Genetics 163:735-746(2003).
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STRAIN=cv. Ab-7, cv. Ang-0, cv. Bg-4, cv. Bla-2, cv. Bur-0, cv. Cv. Co.1, cv. Ct-1, cv. Cvi-0, cv. D2-9, cv. Fm-17, cv. G2-1, cv. Gott-20, cv. Ga-6, cv. Hs-12, cv. Kas-1, cv. Kn02, cv. Mt-0, cv. Tamm-17, cv. Tsu-0, cv. Po-1, cv. Pog-0, cv. Pu-8, cv. Rb, Ms-D, man-17, cv. Tsu-0, cv. War-0, cv. War-0, cv. War-0, cv. War-0, cv. Man-0, and cv. Zu-0, man-17, cv. Tsu-0, cv. Man-0, and cv. Zu-0, man-17, cv. Tsu-0, cv. Man-0, and cv. Zu-0, man-17, cv. Tsu-0, cv. Man-0, and cv. Zu-0, cv. Ms-0, cv. Man-0, and cv. Zu-0, cv. Ms-0, cv. Man-0, and cv. Zu-0, cv. Ms-0, c
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=21231631; PubMed=11333251;
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STRAIN-cv. Columbia;
MEDLINE-95007758; PubMed=7923358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease resistance genes.";
Science 265:1856-1860(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics 158:439-450(2001).
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                                                        NCBI_TaxID=3702;
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Prishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

A Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,

Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

A Latrelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,

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A Nelson J., Spieth J., Ryan E., Dante M., Pepin K., Hillier L.W.,

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Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,

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A Matolius B., Zidanic M., Strong C., Showher M., Matero A., Shah R.,

A Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,

Chen E., Marra M.A., Marilensen R., McCombie W.R.;

"Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
PubMed=11910074; DOI=10.1126/science.1071006;
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"Molecular recognition of pathogen attack occurs inside of plant cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21071235; PubMed=11204781; Axtell M.J., McNellis T.W., Mudgett M.B., Hsu C.S., Staskawicz B.J.; "Mutational analysis of the Arabidopsis RPS2 disease resistance gene and the corresponding pseudomonas syringae avrRpt2 avirulence gene."; Mol. Plant Microbe Interact. 14:181-188(2001).
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MEDLINE-20307433; PubMed=10849351;
Leister R.T., Katagiri F.;
"A resistance gene product of the nucleotide binding site -- leucine rich repeats class can form a complex with bacterial avirulence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGENESIS OF 38-LEU--THR-40; LYS-188; THR-189; THR-190 AND 262-GLU-GLU-263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 93:15497-15502(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTANTS 204C; 205C; 206C; 209C; 210C AND 211C.
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Plant J. 22:345-354(2000).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: Belongs to the disease resistance NB-LRR family.
-i- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
-i- SIMILARITY: Contains 1 NB-ARC domain.
-i- DATABASE: NAME-NIB-LRRS.
-i- DATABASE: NAME-NIB-LRRS.
                                                                                                     AvrRpt2 and modulates RPS2-mediated resistance.";

Cell 112:379-389(2003).

-!- FUNCTION: Disease resistance (R) protein that specifically recognizes the AvrRpt2 type III effector avirulence protein from Pseudomonas syringae. Resistance proteins guard the plant against pathogens that contain an appropriate avirulence protein via an indirect interaction with this avirulence protein. That triggers a defense system including the hypersensitive response, which restricts the pathogen growth. Acts via its interaction with RIN4, and probably triggers the plant resistance when RIN4 is degraded
                                                                                                                                                                                                                                                                                                                                  At4g26090.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Cheuk R., Chen G.H., Dale J.M., Hayashizaki Y., Huuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
                                                                                                                                                                                                                                                                                                                       SUBUNIT: Interacts indirectly with RIN4. Found in a complex with
                                                                        Mackey D., Belkhadir Y., Alonso J.M., Ecker J.R., Dangl J.L.;
"Arabidopsis RIN4 is a target of the type III virulence effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 49; DB 1; Length 909; 55.6%; Pred. No. 96; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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                                                      MEDLINE=22469032; PubMed=12581527
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Cell 112:369-377(2003).
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Best Local Similarity
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Rasko D.A., Ravel J., Oekstad O.A., Helgason B., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.; The genome sequence of Bacilius cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXOl."; Nucleac Acids Res. 32:977-988(2004).
EMBL; AEO17268; AAS40100.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AE017355; AF62000.1; -. Hypothetical protein. SEQUENCE 450 AA; 52210 MW; 2B10A6A1DC93A199 CRC64;
  Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis serovar konkukian str. 97-27.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
Bacillus thuringiensis serovar konkukian.
NCBI _TaxID=281309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
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SEQUENCE 450 AA; 52152 MW; B7B33677CFC5C88C CRC64;
                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheical protein.
0RFNames=BF9727_0987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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57.1%; Pred. No. 66;
tive 3; Mismatches 3
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Pred. No. 66;
3; Mismatches
    Score 48; DB 2;
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                            63;
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Best Local Similarity 57.1%; Pred. No. 6
Matches 8; Conservative 3; Mismatch
                                                                                                                                                                                                                                                           PRT;
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    49.0%;
                            69.2%;
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85 EYKLYNRODSTIVD 98
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OrderedLocusNames=BCE1170;
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321 NYKLYNKNSLFIK 333
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Best Local Similarity 57...
Best Local Similarity 57...
8; Conservative
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                                                 Conservative
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                       Best Local Similarity
Matches 9; Conserv
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    Query Match
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Q73C96;
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Q6HM95
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                                                                                                                                                                                      Gaps
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
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MEDLINE=99102612; PubMed=9847359;
MEDLINE=99102612; PubMed=9847359;
MEDLINE=99102612; Rock D.L.;
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                                                                                                                                       2; Length 909
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis ORF clones.";
Submitred (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BT005972, A0054907. 1;
SEQUENCE 909 AA; 104640 MW; D279B6E30E49D640 CRC64;
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Melcher U.K., Sha Y., Davis R.E., Fletcher J.;
Melcher U.K., Scoot of the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1313-421, AAF18308.1; -.
SEQUENCE 394 AA; 47061 MW; DOD063462F452CF9 CRC64;
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J. Virol. 73:533-552(1999).
EMBL, AF063866; AAC97678.1; -.
PIR; T28318; T28318.
Hypothetical protein.
SEQUENCE 430 AA; 51002 WW; E29A290589066780 CRC64;
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01-UN-2003 (TrEMBLrel. 24, Last sequence update)
Hypothetical protein MSV157.
Mane=MSY157;
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Last annotation update)
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Viruses; ssDNA viruses; Inoviridae; Plectrovirus.
NCBI_TaxID=93224;
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Pred. No. 96;
3; Mismatches
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(TrEMBLrel. 13, I
(TrEMBLrel. 19, I
                                                                                                                                       Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
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Virus Genes 20:47-56(2000).
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Best Local Similarity 64.39
Conservative
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Q9QTH9
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Bacillus cereus (strain ATCC 10987).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Matches 8; Conservative
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Matches 8; Conserv
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SEQUENCE FROM N.A.
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A Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E. Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
A Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
Hanna P.C., Kolstoe A.-B., Friedlander A.M., Koehler T.M.,
T. "The genome sequence of Bacillus anthracis Ames and comparison to
Closely related bacteria.";
L. Nature 423:81-86(2003).
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
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Hitchcock P., Jackeon P., Keim P., Longmire J., Lucas S., Okinaka R.,
Richardson P., Rubin E., Tice H.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
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                                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
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Submitted (MAX-2004) to the EMBL/GenBank/DDBJ databases
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.450 AA; 52228 MW; E74D611E23BD9B62 CRC64;
                                                                                                                                                                                                          OrderedLocusNames=BA1073, BAS1002; ORFNames=GBAA1073;
                                                                                                                    Q81UZ0; Q61ZA5; Q6KW36; 01-UN-2003 (TEMBLrel. 24, Created) 01-UN-2003 (TEMBLrel. 24, Last sequence update) 01-QCT-2004 (TEMBLrel. 28, Last annotation update) Hypothetical protein.
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(TrEMBLrel. 27, I
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STRAIN=Ames / isolate 0581;
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Conservative
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RESULT 15
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STRAIN-Ames 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.; Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AR017334, AA730173.1;
SEQUENCE 450 AA; 52228 MW; E74D611E23BD9B62 CRC64;
PubMed=14960714;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Touresse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Fouts D.E., Trasser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1."; Nucleic Acids Res. 32:977-988(2004).
EMBL; AB017268; AAS40100.1; -.
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Bacteria, Firmicutes; Bacillales; Bacillus;
Bacillus cereus group; Bacillus anthracis.
                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 450 AA; 52152 MW; E7E33677CFC5C88C CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
05-0TL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase D (EC 2.7.1.37).
Name-spkb; OrderedLocusNames=all0776;
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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01-JUN-2004 (TrEWBLrel. 27, Last sequence update)
1-JUN-2004 (TrEWBLrel. 27, Last annotation update)
Hypothetical protein.
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PRELIMINARY;
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   SXC OCC CE DATA
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                                                                                                                                                                                                                                 MEDLINE=96127529; PubMed=8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
Sugiura S.;
Sugiura S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
-I- CAPALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.cib.ch).
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            MEDLINE=22158630; PubMed=12168951; Kamei A., Yuasa T., Geng X., Ikeuchi M.; Ramei A., Yuasa T., Geng X., Ikeuchi M.; Biochemical examination of the potential eukaryotic-type protein kinase genes in the complete genome of the unicellular Cyanobacterium synechocystis sp. PCC 6803."; DNA Res. 9:71-78(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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STRAIN-Ames / isolate Porton;
MEDLINE-22608414; PubMed=12721629; DOI=10.1038/nature01586;
MERLINE-22608414; PubMed=12721629; DOI=10.1038/nature01586;
MEAG T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D64005; BAAL0726.1; -
PIR; S77034; S77034.

FINTERPORTO: IPR01009; Kinase like.

InterPro; IPR000019; Prot kinase. I
FroDom; PF00069; Pkinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; I.
PROSITE; PS00107; PROTEIN KINASE DOM; I.
PROSITE; PS00108; PROTEIN KINASE ST; I.
ATP-binding; Complete proteome; Serine/threonine-protein kinase;
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NCBI_TaxID=1392,
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01-JUN-2003 (TERMBLrel. 24, Created)
01-JUN-2003 (TERMBLrel. 24, Last sequence update)
01-OCT-2004 (TERMBLrel. 28, Last annotation update)
Techoic acid ABC transporter, ATP-binding protein.
OrderedLocusNames=BA5510, BAS5118; ORFNames=GBAA5510;
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ATP (By similarity).
ATP (By similarity).
By similarity.
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3; Mismatches
SEQUENCE FROM N.A., AND CHARACTERIZATION.
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40 40 AT
136 136 By
505 AA; 55213 MW;
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58 KLFEKEASVLEDLGE 72
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Best Local Similarity 60.0
Matches 9; Conservative
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23
40
136
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SEQUENCE
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BINDING
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081K31
LD 081K3
AC 081K3
DT 01-JU
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RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARARARA RARARA RARA
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.; Longmire J., Lucas S., Okinaka R., Submitted (JAN-2004) to the ENBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; ABC1734; AAT34652.1; -.
EMBL; AE017225; AAT57407.1; -.
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Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Colonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Pererson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Flazen A., Cline R.T., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolscoe A.-B., Fraser C.M.;

"The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0000166; P:nucleotide binding; IEA.
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Bacteria, Firmicutes, Bacillales, Bacillus, Bacillus cereus group, Bacillus anthracis.
NCBI_TAXID=261594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
Techoic acid ABC transporter, ATP-binding protein.
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InterPro; IPR001593; ABA_ATBABA.
InterPro; IPR001452; SH3.
InterPro; IPR001642; SH3.
InterPro; IPR001645; SH3.
Probom; PP000006; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PR051TF; PS0021; SH3b; 1.
PR051TF; PS00211; ABC_TRANSPORTER_1; UNGNOWN_1.
PR051TF; PS00993; ABC_TRANSPORTER_2; 1.
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SEQUENCE FROM N.A.
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CHAIN
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                                                                               Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S., Fraser C.M.; Submitted comparative genomics."; Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases. EMBL, ARD1334; AAT34652.1; -. SEMBL, SEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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EMBL; AJ237804; CAB44055.2; -. GO; GO:0019021; Cintegral to membrane; IEA. GO; GO:0019021; C:viral capsid; IEA. GO; GO:0019031; C:viral envelope; IEA. GO; GO:0019031; C:viral GO]. GO:0019031; C:viral envelope; IEA.
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Coat protein; Glycoprotein; Polyprotein; Transmembrane
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49.0%; Score 48; DB 2; Length 549;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Immunodeficiency virus 1.
Viruses; Retrold viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90885 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YKLYNKNSSTLKDL 17
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Best Local Similarity 64...
Best Local Similarity 64...
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Pfam; PF00517; GP41; 1.
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802 AA;
SEQUENCE FROM N.A. STRAIN=Ames 0581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11676;
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01-MAY-2000 (
01-JUN-2003 (
ENV protein (
Name=env;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MP411;
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SEQUENCE
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090BY6;
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090204
DD 001-MA
DT 01-MA
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Q9QBY6
    SERFERS
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MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Rogers Y.H., Blazej R.G., Champe M., Ffeiffer B.D.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., Berman B.P., Bhandari D., Bolshakov S.,
Besson K.Y., Benos P.V., Berman B.P., Brottier P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Autris K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Abril W., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Abril W., Cawley S., Dahlke C., Bayamport L.B., Dick S.,
Abril M., Cawley S., Dahlke C., Bayamport B.C., Dunn P.,
Abril M., Cawley S., Bhilke C., Bayamport B.C., Dunn P.,
Abril M., Gangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Alosen K., Goorell J.H., Gu Z., Gebart W.M., Glasser K.,
Alaris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
MEDLINE=20122179; PubMed=10659053;
Triques K., Bourgeois A., Vidale N., Mpoudi-Ngole E.,
Mulanga-Kabeya C., Nzilambi N., Torimiro N., Saman E., Delaporte E.,
                                                                                                                                                   "Near-full-length genome sequencing of divergent African HIV type 1 subtype F viruses leads to the identification of a new HIV type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.0%; Score 48; DB 2; Length bb. 49.0%; Pred. No. 1.38+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEF protein.
ENV protein.
4B091F2348930F4C CRC64;
                                                                                                                                                                                                                                                           AIDS Res. Hum. Retroviruses 16:139-151(2000).

EMBL, AJ749218; CAB58986.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0009198; Fishructural molecule activity; IEA.
InterPro; IPR000328; ENV GP41.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-UU-2004 (TrEMBLrel. 27, Last annotation update)
CG4866-PA (RE57564p).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96574 MW;
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les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                       subtype designated K.";
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Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mont S.M., Moy M., Murphy B., Murphy L., Muzhy D.M., Nelson D.E., Molson D.R., Nelson D.R., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Sampson M., Skupski M.P., Shen H., Shue B.C., Staden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B.C., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X.Y., Wassarman D.A., Weinstock G.M., Zhao G., Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
MEDLINE=22436065; PubMed=12537568;
MEDLINE=22436065; PubMed=12537568;
Medline=15., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacifer B.D., Richards S., Sodergren E.J.,
Weinstrak R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22426069; PubMed=12537572;
Mistra B., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J. K. Senso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003803; AAF57847.2; -.
EMBL; AY071534; AAL49156.1; -.
IntAct; Q9V832; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomics perspective.";
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FlyBase; FBgn0034232; CG4866.

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                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132, PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                             ö
                                                                         Length 181;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046729; AAH46729.1; -.
InterPro; IFR006434; HAD SF-IE.
Pfam; PF05822; UMPH-1; 1.
                                          PROSITE; PS50889; S4; 1.
SEQUENCE 181 AA; 21304 MW; 1EAD137DEC9A54AA CRC64;
                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                       48.0%; Score 47; DB 2;
47.4%; Pred. No. 37;
tive 3; Mismatches
                                                                                                                                                                                        294 AA.
                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
GO; GO:0003723; F:RNA binding; IEA.
InterPro; IPR002942; S4.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
                                                                                                                                                                                        PRT;
                                                                                                                  1 RSDYKLYNKNSSTLKDLGE 19
                                                                                                                              41 REDYTKYNKLSREIRELAE 59
                                                                                                                                                                                                                                        LOC398553 protein (Fragment).
Name=LOC398553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initiative.";
Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.";
                                                                                   Local Similarity 47.4 nes 9; Conservative
                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
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                                                                          Query Match
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Matches
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Gaps

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Q7MV25

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RESULT 25 Q7MV25

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STRAIN=S2 / LL;
Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J., Conway de Macario E., Dodsworth J., Gillett W., Graham D.E., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T., Major E., Porat I., Overbeek R., Palmeiri A., Rouse G., Saenphimmachak C., Soell D., Whitman W.B., Larimer F.W., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the mesophilic hydrogenotrophic methanogen Methanococcus maripaludis."; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BX957223; CAF31084.1; -.
                                                                                                                                                                                                                                                                                                                     Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 46; DB 2; Length 268; 53.3%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
methanogen Methanococcus maripaludis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX957223; CAF31084.1;
GQ; GQ: 00046629; F: 1yase activity; IEA.
GQ; GQ: 0004664; F: prephenate dehydratase activity; IEA.
InterPro; IPR002912; ACT.
InterPro; IPR00837; PDT ACT.
InterPro; IPR008037; PDT ACT.
Ffam; PF01842; ACT; 1.
Pfam; PF018000; PDT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
ORFNames=BG1071,
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Pirmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                            268 AA; 30314 MW; 44034DD35B0E1155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanococcaceae; Methanococcus.
NCBI TaxID=39152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 268 AA; 30314 MW; 44034DD35B0E1155 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                     46.9%; Score 46; DB 2; 53.3%; Pred. No. 80;
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PROSITE, PS00888; PREHENATE_DEHYDR_2; 1.
COMPLE PICTECOMP; 1/2488.
SEQUENCE 268 AA; 30314 MW; 44034DD35B
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Best Local Similarity 53.3%
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus maripaludis.
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Matches 8; Conservative
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EMBL: ABO1776; AAQ66363.1; -.

Complete protecome; Hypothetical protein.

SEQUENCE 720 AA; 81982 MW; DOFF2762EBE0901D CRC64;
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Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                          Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the mesophilic hydrogenotrophic
                                         Query Match
48.0%; Score 47; DB 2; Length 294;
Best Local Similarity 90.0%; Pred. No. 61;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.0%; Score 47; DB 2; Length 720; 57.1%; Pred. No. 1.6e+02; ive 3; Mismatches 3; Indels
  7291143809896760 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanococcaceae, Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amnotation update)
Prephenate dehydratase (EC 4.2.1.51).
Name=pheA, OrderedLocusNames=WMP1528;
                                                                                                                                                                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                              720 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=W83;
MEDLINE=22829867; PubMed=12949112;
  294 AA; 33984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 57.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :| ||| | ::|||
47 EYDLYNPNGTSLKD 60
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                                                                                                                                                                                                                                                                                                                                                                                                        OrderedLocusNames=PG1283;
                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                     205 YNKNSSVLKD 214
                                                                                                                              7 YNKNSSTLKD 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=837;
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  SEQUENCE
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RESULT 26
06LX25
AC 06LX21
AC 06LX22
AC 06LX22
DT 05-JUJ

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Neurospora crassa.
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SEQUENCE FROM N.A.
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                                   NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Uspl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   homolog
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                               MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Maur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Overbeek R., Kyrpides N.C.; Ponstein M., Ehrlich S.D., Overbeek R., Kyrpides N.C.; Bacillus sequence of Bacillus cereus and comparative analysis with Bacillus anthracis.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NCTC 11168;
MEDLINE=2012; PubMed=10688204; DOI=10.1038/35001088;
MEDLINE=2012; PubMed=10688204; DOI=10.1038/35001088;
Barkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                                                                                                                                            Length 450;
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                                                                                                                                                                                          Query Match
46.9%; Score 46; DB 2; Length 450
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 4; Mismatches 3; Indels
                                                                                                                               Nature 423:87-91(2003).
EMBL; AE017001; AAP08058.1; -.
Hypothetical protein.
SEQUENCE 450 AA; 52193 MW; B93F7BE8EFF57545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome, Hypothetical protein.
SEQUENCE 465 AA; 56341 MW; E14E40D639E8D5C1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Cj0030.
OrderedLocusNames=Cj0030;
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                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                              PRT;
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EYKMYNRQDSTIVD 98
                                                                                                                                                                                                                                            3 DYKLYNKNSSTLKD 16
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Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
NCBI_TaxID=226900;
                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      -OCT-2000
                     SEQUENCE
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Q8XOB9
ID Q8XOE
AC Q8XOE
DT 01-MA
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
enriched library, clone:B430116N19 product:UBIQUITIN-SPECIFIC PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Adipose; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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                                                                                                                                                                          Holland R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Adipose;
STRAIN=C1085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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Eukaryota, Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.9%; Score 46; DB 2; Length 530; 75.0%; Pred. No. 1.6e+02; Live 2; Mismatches 1; Indels
                                                                                                                                      SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B.,
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                             German Neurospora genome project; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, ALG70007; CAD21310.1; -.. InterPro; IPR001810; F-box. InterPro; IPR01811; FBOX; 1.. Hypothetical protein. SeQUENCE 530 AA; S9352 MW; 70382EE15F71BB9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Adipose;
MEDLINE=99279253; PubMed=10349636;
METRING P., Hayashizak' Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Adipose;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.00,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 YRLFNKFSSTLK 369
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Mus musculus (Mouse)
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   $\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac{1}{2}$\frac
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C STRAIN=CS7BL/GJ; TISSUE=Adipose;
A Adachi J., Aizawa K., Akimura T., Broo H., Carninci P.,
Adachi J., Aizawa K., Haragaki T., Hara A., Hashizume W.,
A Fukuda S., Furuno M., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Raswak D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
Submitted (App. 2002) to the BEL/GenBank/DDBJ databases.
EMBL; AKOSOBS J., EAG38059.1; -
                                                         SEQUENCE FROM N.A.

SITALN=C57BL/61; TISSUE=Adipose;
STRAIN=C57BL/61; TISSUE=Adipose;
STAIN=C30330913; PubMed=11076861;
A MEDLINE=20330913; PubMed=11076861;
A Konno H., Akiyama J., Niehi K., Kiteunai T., Tashiro H., Itoh M., Axamura S., Hazama M., Niehine T., Harada A., Sumi N., Ishil Y., Matamura S., Hazama M., Niehine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikagami T., Kashiwagi K., A Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MGD; MGI:2385198; Uspl.
GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0004221; F:peptidase activity; IEA.
GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
GO; GO:0006511; P:ubiquitin chiolesterase activity; IEA.
GO; GO:0006511; P:ubiquitin dependent protein catabolism; IEA.
InterPro; IPR001394; CytC heme_BS.
InterPro; IPR001394; PeptIdase_C19.
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Last annotation update)
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PROSITE; PS00973; UCH_2 1; 1.
PROSITE; PS00973; UCH_2 2; 1.
PROSITE; PS50235; UCH_2 2; 1.
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 50.v.
9; Conservative
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Mus musculus (Mouse).
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SEQUENCE
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089VE17
10 08VE17
08VE17
08VE10
01-MA
DT 01-MA

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RC virgin mouse. Taken by biopsy.;

RX Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altechul S.F., Zeeborg B. Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Altechul S.F., Zeeborg B. Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Diafrchenko L., Marueina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Shevchenko Y., Bouffard S., Sanchez A.,

Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rahay J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RY "Generation and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human
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WEDLINE-22388257; PubMed-12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Mammary tumor. Metallothionien-TGF alpha model. 10 month virgin mouse. Taken by biopsy.;
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GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
GO; GO:0005511; F:ubiquitin-dependent protein catabolism; IEA.
InterPro; IPR001345; CytC heme_BS.
InterPro; IPR001394; Peptidase_C19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020007; AAH20007.1; -.
HSSP; Q93009; 1NBF.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00443; UCH; 1.
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SEQUENCE
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Rischul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Daybins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Allalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., A. Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermococcus sp. (strain TY).
Archaea, Buryarchaeota, Thermococci, Thermococcales, Thermococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98094267; PubMed-9434178;
Niehbus F., Frey B., Antranikian G.;
"Cloning and characterisation of a thermostable alpha-DNA polymerase
from the hyperthermophilic archaeon Thermococcus sp. TY.";
Gene 204:153-158(1997).
                                                                                                                                                                                                                                                                STRAIN=FVB/N;
TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
virgin mouse. Taken by biopsy.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL) BC018179; AMH18179.1; -.
HSSP; Q93009; INBF.
MGD; MG1:2385198; Usp1.
GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
GO; GO:0004221; F:ubiquitin-thiolesterase activity; IEA.
GO; GO:0004221; F:ubiquitin-thiolesterase activity; IEA.
GO; GO:000621; F:ubiquitin-dependent protein catabolism; IEA.
InterPro; IPR001394; Peptidase_C19.
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                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PF00443; UCH; 1.
PROSITE; PS00190; CYTOCHROME C; UNROWN 1.
PROSITE; PS00973; UCH 2 1; 1.
PROSITE; PS00973; UCH 2 2; 1.
PROSITE; PS00235; UCH 2 2; 1.
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                                                                                                                                                                                                              and mouse cDNA sequences."
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Best Local Similarity
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033845;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                  PTM: This protein undergoes a protein self splicing that involves a post-translational excision of the three intervening regions (inteins) followed by peptide ligation.
SIMILARITY: Belongs to the DNA polymerase type-B family.
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MEDLINE=22072559; PubMed=12076768;
Blair P.L., Kappe S.H., Maciel J.E., Balu B., Adams J.H.;
Plasmodium falciparum MAEBL is a unique member of the ebl family.";
Mol. Biochem. Parasitol. 122:35-44 (2002).
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DNA polymerase, 2nd part (Potential).
Intein II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase, 3rd part (Potential).
Intein III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase, 1st part (Potential).
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MW; All3A8BC57EB9CB3 CRC64;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Pred. No. 5.9e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TICETETO; IFROJATO; POL B: 4.

PÉAM; PF03104; DNA_DOL B: 4.

PEAM; PF03104; DNA_DOL B: 4.

PENINTS; PR00379; INTEIN.

TIGREAMS; TIGR01443; Intein. Nerm; 3.

TIGREAMS; TIGR01443; Intein. Nerm; 3.

TIGREAMS; TIGR0192; DOL2; 2.

PROSITE; PS00116; DNA_DOLYMERASE B; FALSE_NEG.

PROSITE; PS50819; INTEIN. C. TER; 3.

PROSITE; PS50819; INTEIN. ENDONUCLEASE; 2.

PROSITE; PS50817; INTEIN. NER; 3.

Autocatalytic cleavage; DNA_replication; DNA-binding; DNA-directed DNA_DOLYMETABE; Endonuclease; Hydrolase; Protein splicing; Transferase.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006172; DNA_pol_B.
InterPro; IPR006133; DNA_pol_B exo.
InterPro; IPR006134; DNA_pol_B_region.
InterPro; IPR006142; INTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004042; Intein endonuc.
InterPro; IPR006141; Intein_S.
InterPro; IPR004578; Pol2.
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1161 KLYNENPNVLKDM 1173
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Best Local Similarity 61.5
Matches 8; Conservative
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770 85
856 139
1393 144
1442 159
1599 182
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SEQUENCE FROM N.A.
MEDLINE-22072559; PubMed=12076768;
Blair P.L., Kappe S.H., Maciel J.E., Balu B., Adams J.H.;
"Plasmodium falciparum MAEBL is a unique member of the ebl family.";
Mol. Biochem. Parasitol. 122:35-44(2002).
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MEDLINE=22072559; Pubmed=12076768;
Blair P.L., Kappe S.H., Maciel J.E., Balu B., Adams J.H.;
Plasmodium falciparum MMEBL is a unique member of the ebl family.";
Mol. Biochem. Parasitol. 122:35-44(2002).
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22077637; Pubmed=12082132;
Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 19:1128-1142(2002).
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Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships Of conserved cysteine-rich motifs
adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 19:1128-1142(2002).
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Blair B.L., Kappe S.H.I., Maciel J.E., Balu D.J., Adams B.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY042084; AAQ73468.1; -.
InterPro; IPR008957; FN III-like.
SEOUENCE 2019 AA; 239410 Mw; A626F2C684C08785 CRC64;
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Blair B.L., Kappe S.H.I., Maciel J.E., Balu D.J., Adams B.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY420084 AAQ73468.1; -.
SEQUENCE 2019 AA; 239410 MW; A626F2C684C08785 CRC64;
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Erythrocyte binding protein 2.
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53.3%; Pred. No. 6.5e+02;
tive 3; Mismatches 4;
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551 TDNKLYNNNNQKIKD 565
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Matches 8; Conservative
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Best Local Similarity
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                                      NCBI_TaxID=5833;
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AAQ73468;
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Blair P.L., Kappe S.H., Marclel J.E., Balu B., Adams J.H.;
"Plasmodium falciparum MABEL is a unique member of the ebl family.";
Mol. Biochem. Parasitol. 122:35-44(2002).
                                                    Michon P., Stevens J.R., Kaneko O., Adams J.H.; "Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites."; Mol. Biol. Evol. 19:1128-1142 (2002).
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"Byolutionary relationships of conserved cysteine-rich motifs
adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 19:1128-1142 (2002).
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                 46.9%; Score 46; DB 2; Length 2006; 53.3%; Pred. No. 6.5e+02; tive 3; Mismatches 4; Indels
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53.3%; Pred. No. 6.5e+02;
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Blair B.L., Kappe S.H.I., Maciel J.E., Balu D.J., Adams B
Submitred (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY042084; AAQ73469.1; -
SEQUENCE 2006 AA; 237620 WW; EE75EF42E2BF767D CRC64;
                                                                                                                                                                        Blair B.L., Kappe S.H.I., Maciel J.E., Balu D.J., Adams Esubairted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY042084, AAQ13469-1. SEQUENCE 2006 AA, 237620 WW, EE75EF42E2BF767D CRC64;
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Last sequence update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Erythrocyte binding protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2006 AA
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MEDLINE=22077637; PubMed=12082132;
                                      LINE=22077637; PubMed=12082132;
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(TrEMBLrel. 27, Las
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binding protein 2.
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551 TDNKLYNNNOKIKD 565
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551 TDNKLYNNNNQKIKD 565
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nes 8; Conservative
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Best Local Similarity
                  SEQUENCE FROM N.A.
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Q7K5QS;
Q5-JUL-2004 (
05-JUL-2004 (
05-JUL-2004 (
Erythrocyte b
Name=maebl;
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AAQ73469;
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Q7K5Q5
ID Q7K5Q
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MEDLINE=22255705; PubMed=12368864;
Gardner M.J. Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Gardner M.J., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.S., Nene V., Shallon S.J. Sub B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Morfadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.;
"Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Blair P.L., Kappe S.H., Marclel J.E., Balu B., Adams J.H.;
"Plasmodium falciparum MABEL is a unique member of the ebl family.";
Mol. Biochem. Parasitol. 122:35-44(2002).
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Last annotation update)
1 (Chimeric erythrocyte-binding protein
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MEDLINE=22077637; Pubmed=12082132;
Michon P., Stevens J.R., Kaneko O., Adams J.H.;
"Evolutionary relationships of conserved cysteine-rich motifs in adhesive molecules of malaria parasites.";
Mol. Biol. Evol. 19:1128-1142(2002).
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                                                                                                                                                                                                 MAEBL, putative.
OKFNames=PP11 0486;
Plasmodium falciparum (isolate 3D7).
Bukaryota, Alvedata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.9%; Score 46; DB 2; Length 2055; 53.3%; Pred. No. 6.6e+02; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; ARO14843; AAN38066.1; -.
HSSP; P04268; 11C2.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004972; F:receptor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPror; IPR008602; Duffy binding.
Pfam; PF05424; Duffy binding.
SEQUENCE 2055 AA; 243211 MW; 783F48BB7286B1F3 CRC64;
                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                          PRT; 2055 AA
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551 TDNKLYNNNNOKIKD 565
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01-JUN-2002 (TrEMBLrel. 21,
05-JUL-2004 (TrEMBLrel. 27,
Erythrocyte binding protein
                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
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Plasmodium falciparum.
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Best Local Similarity 53.3.
                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 419:498-511 (2002)
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01-MAR-2003
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08T5C7
1D Q8T5C
AC Q8T5C
AC Q8T5C
AC Q8T5C
DT 01-JU
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DT 01-JU
DT 05-JU
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GN MAEBI
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CO EUKA
OX NOCBI
RR SEQT
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QBIHP3
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MEDLINE=22155635; PubMed=12165387;
Ghai M., Dutta S., Hall T., Freilich D., Ockenhouse C.;
Ghai M., Dutta S., Hall T., Freilich D., Ockenhouse C.;
Identification, expression, and functional characterization of MABBL,
a sporozoite and asexual blood stage chimeric erythrocyte-binding
protein of Plasmodium falciparum.";
Mol. Blochem. Parasitol. 123:35-45(2002).
BMBL, AX042084; AAL10509.1;
BMBL, AF040002; AAM90625.1;
BMBL, AF060002; AAM90625.1;
BMBL, AF060002.
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Blair B.L., Kappe S.H.I., Maciel J.E., Balu D.J., Adams B.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2055;
                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPRO08602; Duffty binding.
Ffam; PF05424; Duffty binding; 1.
SEQUENCE 2055 AA; 243211 MW; 783F48BB7286B1F3 CRC64;
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551 TDNKLYNNNNQKIKD 565
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Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein November 24, 2004, 09:11:44 Run on:

; Search time 15.6957 Seconds (without alignments)
116.473 Million cell updates/sec

US-09-719-379A-4 98 Perfect score:

1 RSDYKLYNKNSSTLKDLGE 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pirl:* 3: pir2:* 4: pir4:* 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

35	Description	outer membrane pro	orfl protein - fow	disease resistance	ORF MSV157 hypothe	protein kinase pkn	hypothetical prote	probable polyprote	holliday junction	hypothetical prote	hypothetical prote	+	hypothetical prote		hypothetical prote	uncharacterized co	hypothetical prote	beta-N-acetylhexos	26S proteasome reg	ATP-dependent DNA	hypothetical prote	p74 protein - Auto	occlusion-derived	trypsin inhibitor	hypothetical prote	conserved hypothet	hypothetical prote	ornithine carbamoy	probable chromatin	serine/threonine-s
SUMMARIES	ID	C64187	A60013	A54809	T28318	S77034	A81419	G85055	B90594	T49066	S50295	S46177	A69824	C84164	S52703	H97060	H71854	B70100	S59773	H97040	H70330	WMNV74	C72867	JH0607	D90400	B70020	F84951	OWBS	T38471	860159
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å	Query	88.8	50.0	50.0	49.0	49.0	46.9	45.9	•	44.9		44.9	43.9	٠	43.9	•	•	43.9	•	•	43.9	43.4	43.4	42.9	42.9	42.9	42.9			
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ankyrin-like prote	beta-lactamase cla	probable ubiquitin	hypothetical prote	hypothetical prote	autotransporter pr	male-enhanced anti	DNA segregation AT	adenosinetriphosph	hypothetical prote	N-methyl-D-asparta	hypothetical prote	ferrous ion transp	hypothetical prote	amino acid ABC tra	leucine dehydrogen
T48596	E97245	T17309	T25827	T08605	AD3203	T42722	B97355	S67483	E86212	847555	F70106	D86648	B71713	E69996	F72020
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591	739	785	831	947	1035	1325	1498	1553	615	1464	125	152	193	270	351
42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.3	42.3	41.8	41.8	41.8	41.8	41.8
42	42	42	42	42	42	42	42	42	41.5	41.5	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Outer membrane protein A homolog - Haemophilus influenzae (strain Rd KW20)
C.Species: Haemophilus influenzae
C.Species: Haemophilus
C.Species: Haemophi
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A;Residues: 1353 <TIGR> A;Cross-references: UNIPROT:P43840; GB:U32796; GB:L42023; NID:g1574086; PIDN:AAC22819.1; C;Superfamily: outer membrane protein A

Gaps ö Length 353; 1; Indels Query Match
88.8%; Score 87; DB 2; L
Best Local Similarity 89.5%; Pred. No. 5.4e-06;
Matches 17; Conservative 1; Mismatches 1;

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132 RSDYKLYNENSSTLKKLGE 150 1 RSDYKLYNKNSSTLKDLGE 19 g ò

Orfi protein - fowlpox virus

C;Species: fowlpox virus

C;Species: fowlpox virus

C;Accession: A60013

R;Kumar, S; Boyle, D.B.

Virus Res. 15, 175-186, 1990

A;Title: Mapping of a major early/late gene of fowlpox virus.

A;Accession: A60013

A;Status: preliminary

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-167 «KUM» A;Cross-references: UNIPROT:Q05569; GB:X52461; NID:g62320; PIDN:CAA36694.1; PID:g62321 C;Superfamily: RNA polymerase subunit 19, poxvirus type

Gaps ö Length 167; 4; Indels 50.0%; Score 49; DB 2; 38.9%; Pred. No. 2.5; tive 7; Mismatches Query Match Best Local Similarity 38.99 Matches 7; Conservative

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2 SDYKLYNKNSSTLKDLGE 19 ::||| |:: :: |:||

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protein kinase pknA (EC 2.7.1.-), 55K - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sl10776
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S77034
C;Accession: S77034
S;Kanoko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-505 «KAN»
A;Cross-references: UNIPROT:P54735; EMBL:D64005; GB:AB001339; NID:g1001779; PIDN:BAA1072.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin. C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; WIID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q9PJ81; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7252
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: pknA
C;Superfamily: Synechocygiis sp. protein kinase pknA, 55K; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Cj0030 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: Cj0030
C;Superfamily: Campylobacter jejuni hypothetical protein Cj0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: S74322; MUID:97061201; PMID:8905231 A;Accession: S77034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 2;
Pred. No. 23;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.0%; Score 48; DB 1; 60.0%; Pred. No. 12; ative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: phosphotransferase; protein kinase F; 7-268/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S KLYNKNSSTLKDLGE 19
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KLFEKEASVLEDLGE 72
                                                                                                    321 NYKLYNKNSLFIK 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 60.0.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 69.2.
Best Local 9; Conservative
                                   3 DYKLYNKNSSTLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 YNKNSSTLKDLGE 19
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A; Residues: 1-465 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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G85055
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                                                                                                                  ACCOSSION 13 ASSOCIATION PROBLEM CONTROL 18 AND STATE OF THE STATE OF 
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T28318
ORP MX/157 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28118
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, B.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
J. Virol. 73, 533-552, 1999
J. Virol. 73, 533-552, 1999
J. Aritie: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28318
A;Accession: T28318
A;Accession: T28318
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-430 <AFO>
A;Residues: 1-430 <AFO>
A;Cross=references: UNIPROT:Q9YVT5; EMBL:AF063866; NID:94049647; PIDN:AAC97678.1; PID:94
A;Note: MSV157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
49.0%; Score 48; DB 2; Length 430;
Best Local Similarity 69.2%; Pred. No. 10;
Matches 9; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||| | |: || :||
111 ADYKLCKKVSAILKSIGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SDYKLYNKNSSTLKDLGE 19
   NDYKSYDEDDDSISDIGE 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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Length 262; Indels

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C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004
C;Date: 23-Aug-1995 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: $50295; $51389; $56875; $56876; $57370
R;Miosga, T:; Boles, E.; Schaaff-Gerstenschlaeger, I.; Schmitt, S.; Zimmermann, F.K.
Yeast 10, 1481-1488, 1994
A;Title: Sequence and function analysis of a 9.74 kb fragment of Saccharomyces cerevisia
A;Reference number: $50295; WUID:95176706; PMID:7871887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .Molecule type: DNA
Residues: 1-1058 cMIO>
:Cross-references: UNIPROT:P40856; EMBL:X77923; NID:g640004; PIDN:CAA54892.1; PID:g6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-852 <RAS>
A;Cross-references: EMBL:X85021
R;Niosga, T.; Schaaff-Gerstenschlaeger, I.; Baur, A.; Boles, E.; Chalwatzis, N.; Fournie
submitted to the Protein Sequence Database, September 1995
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;Residues: 1-1058 <MIF>
;Crose-references: EMBL:Z49373; NID:g1008275; PIDN:CAA89392.1; PID:g1008276; MIPS:YJL09
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least 11, 873-883, 1995
least 11, 873-883, 1995
i,jTitle: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, GSH1 and CSD3
i,Reference number: S57357; MUID:96090136; PMID:7483851
i,Accession: S57370
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A,Cross-references: EMBL:X85021
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Rasmussen, S.W. submitted to the EMBL Data Library, February 1995
A;Description: A 37.5 kb region of yeast chromosome X includes the SME1, MEF2, A;Reference number: S53376
A;Accession: S53389
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lypothetical protein YKR028w homolog YJL098w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: nucleic acid sequence not shown; translation not shown
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60.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 6; Indels
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                                                                                                                                                      core 44; DB : red. No. 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V;Alternate names: hypothetical protein J0840
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A'Residues: 1-852 «RAW»
A'Cross-references: EMBL:Z49373; MIPS:YJL098w
                                                                                                                                                           Score 44;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: nucleic acid sequence not shown
                                                                                                                                                               44.9%;
53.3%;
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158 RLTNKPNATIEDLGE 172
                                                                                                                                                                                                                                                                                                                                         5 KLYNKNSSTLKDLGE 19
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A;Map position: 10L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYKLYNKNSSTLKDL 17
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                                                                                                                                                      Query Match
Best Local Similarity 53.3
Matches 8; Conservative
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Best Local Similarity
                               A;Map position: 3
A;Introns: 101/1; 206/3
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probable polyprotein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Reb-2001 #sequence_revision 16-Reb-2001 #text_change 09-Jul-2004
C;Accession: G85055
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: G85055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1017 <STO>
A;Cross_references: UNIPROT:Q9XEB9; GB:NC_001268; NID:g7267198; PIDN:CAB77909.1; GSPDB:CC;Genetics: A74904410
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 holiday junction DNA helicase ruvB [imported] - Mycoplasma pulmonis (strain UAB CTIP)
(5)Species in Mycoplasma pulmonis
(5)Species in Mycoplasma pulmonis
(5)Species in Mycoplasma pulmonis
(5)Species in Mycoplasma pulmonis
(5)Accession: B90594
(6) Arcids Res. 29, 2145-2153, 2001
(7) Arcids Res. 29, 2145-2153, 2001
(7) Arcids Res. 29, 2145-2153, 2001
(8) Arcids Res. 29, 2145-2153, 2001
(9) Arcids Res. 29, 2145-2153, 2001
(9) Arcids Res. 29, 2155-2153, 2001
(9) Arcids Res. 200594
(9) Arcids Res. 200594
(9) Arcids Res. 200594
(9) Arcids Res. 200594
(9) Arcids Res. 2006
(1) Arcids Res. 2007
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O.3-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49066
R;Benses, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, Isubalted to the Protein Sequence Database, April 2000
A;Reference number: Z25014
A;Reference number: Z25014
A;Status: preliminary
A;Residues: 1-262 <BRN>
A;Residues: 1-262 
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A;Experimental source: cultivar Columbia; BAC clone T5P19
C;Genetics:
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ed. No. 74;
Mismatches
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68.8%; Pred. No. 26;
tive 0; Mismatches
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Pred. No.
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936 DTKLFLKSTFDIKDLGE 952
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9, Conservative
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A,Genetic code: SGC3
C,Superfamily: ruvB protein
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Best Local
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Matches
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GSH1 and

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Length 1058;

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C;Accession: C84164
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo. Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danishlas, C.J.; Dennis, P.D.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Hitle: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9HSX1; GB:AE004437; NID:g10579691; PIDN:AAG18679.1; GSPDB:G-
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A;Residues: 1-241 -COLT-
A;Cross-references: UNIPROT:Q03941; EMBL:Z48784; NID:g755782; PIDN:CAA88709.1; PID:g7557'
A;Experimental source: strain AB972
                                                                                                                                               A;Residues: 1-131 «KUN»
A;Cross-references: UNIPROT:PS4605; GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12750.
A;Experimental source: strain 168
C;Genetics:
                               A;Accession: A69824
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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N;Alternate names: hypothetical protein YD9346.07c
C;Species: Saccharomyces cerevisiae
C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52703
R;Oliver, K.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S52697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Vng0040c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                              A;Gene: yhcU
C;Superfamily: Bacillus subtilis hypothetical protein yhcU
A; Reference number: A69580; MUID: 98044033; PMID: 9384377
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A;Map position: 4R
C;Superfamily: conserved hypothetical protein YDR196c
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50.0%; Pred. No. 20;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.9%; Score 43; DB 2; Best Local Similarity 47.1%; Pred. No. 18; Matches 8; Conservative 2; Mismatches
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DYKOVHONLSELEDIG 108
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nes 8; Conservative
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A, Status: preliminary
A, Molecule type: DNA
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                   RESULT 11

probable Ca2+-transporting ATPase (EC 3.6.3.8) - yeast (Saccharomyces cerevisiae)
NiAlecrane names: hypothetical protein THEALLS; hypothetical protein YBR25sw
C; Bace: Saccharomyces cerevisiae
C; Bate: Saccharomyces cerevisiae
C; Cate: Saccharomyces cerevisiae
R; C; Cate: Saccharomyces cerevisiae
R; C; Cate: Saccharomyces C.P.; Kirchrath, L.; Ramezani Rad, M.
A; Reference number: S46175
A; Reference number: S4618; MID: 9274324; PMID: 775471
A; Reference number: S4618; MID: 9274324; PMID: 775471
A; Reference number: S4618; MID: 9274324; PMID: 775471
A; Reference number: S4618; MID: 9274325, PIDN: CAM82529.1; PID: 9547580
C; Generice: S60; PCA1
A; Reference number: S60; Reference number: Reference number: S60; Reference number: S60; Reference number: Reference number: S60; Reference number: Reference number: Reference number: S60; Reference number: Refe
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hypothetical protein yhcu - Bacillus subtilis

c;Species: Bacillus subtilis

c;Species: Bacillus subtilis

c;Accession: A69824

R;Kunst, F; Ogasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C; Eroni, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

A; Brnich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

A;Authors: G.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liuu, H.; Mauda, S.; Maueell

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Mauda, S.; Maueell

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sado, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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284 RMYNRYSSILKNLG 297
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Best Local S
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R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, J. Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Mature 390, 580-586, 1997
A,Authors: Smith, H.O.; Venter, J.C.
A,Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A,Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A,Reference number: A70100; MUID: 98065943; PMID: 9403685
A,Recession: B70100
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-342 <KLE>
A,Residues: 1-342 <KLE>
A,Residues: Last of RESARCO1115; GB: AE000783; NID: G2687879; PIDN: AAC6640
A,Experimental source: strain B31
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Modecule type: DNA
A,Residues: 1-429 «MEL»
A,Cross-references: UNIPROT:Q06103; EMBL:U32445; NID:g914969; PIDN:AAB68078.1; PID:g9149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26S proteasome regulatory particle chain RPN7 - yeast (Saccharomyces cerevisiae)
Althernate names: protein P8283.8; protein YPR108w
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                         Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: MIPS:YPR108w; SGD:S0006312
A;Map position: 16R
C;Keywords: nucleotide binding; P-loop
F;150-157/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July 1995
A;Description: The sequence of S. cerevisiae cosmid
A;Reference number: S59764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 43.9%; Score 43; DB 2; Best Local Similarity 47.6%; Pred. No. 62; Matches 10; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                         43.9%; Score 43; DB 53.3%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :||| || || || || DQELYNELCKKNESKIKELNE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 DYKLYN----KNSSTLKDLGE 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: SGD: RPN7; RPN7; MIPS: YPR108w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 DYKLYNKNSSTLKDL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 DYEYFNKDKSDLVDL
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-609 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S59773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Genetics:
A; Gene: CAC1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Nelson, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 19
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                                                                                                                                                                                                                 RESULT 15
H97060
uncharacterized conserved protein, probable metal-binding CAC1304 [imported] - Clostridiu uncharacterized conserved protein, probable metal-binding CAC1304 [imported] - Clostridiu uncharacterized conserved protein, probable metal-binding CAC1304 [imported] - Clostridiu C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C; Accession: H97060
R; Nolling, J: Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: H97060
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Residues: 1-252 - KUR>
A; Residues: 1-252 - KUR>
A; Residues: 1-252 - KUR>
A; Cross-references: UNIPROT:Q97JH9; GB:AE001437; PIDN:AAK79275.1; PID:g15024234; GSPDB:G A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein jhp1056 - Helicobacter pylori (strain J99)
C; Species: Helicobacter pylori
A; Variety: strain J99
C; Species: Helicobacter pylori
A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C; Date: 12-Sibon, R; Merberg, D.T; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Iveluce 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Reture 37
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Readiduse: 1-263 < ARN>
A; Cross-references: UNIPROT:Q9ZK85; GB:AE001533; GB:AE001439; NID:g4155636; PIDN:AAD0663
A; Experimental source: strain J99
C; Genetics:
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B70100
beta-N-acetylhexosaminidase homolog - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: B70100
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Length 252;
                                       Indels
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                                       3,
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Pred. No. 35;
2; Mismatches
           Pred. No. 34;
                                                                                                                                           175 RSDYIL--ONNSTLVDLYE 191
                                                                                         1 RSDYKLYNKNSSTLKDLGE 19
        63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.9%;
61.5%;
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221 SDFKDYNKSVMTLLD 235
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Best Local Similarity 60.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
        Best Local Similarity
Matches 12; Conserv
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                                                                                            8
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-645 <AYR>
A;Cross-references: UNIPROT:P15963; GB:L22858; NID:g510708; PIDN:AAA66768.1; PID:g559207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Acacia confusa
C;Date: 17-Aug-1992 #sequence revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: JH0607; PN0539; JX0255
R;Hung, C.H.; Lee, M.C.; Lin, J.Y.
Biochem: Blophys. Res. Commun. 184, 1524-1528, 1992
A;Title: Nucleotide sequence of CDNA for Acacia confusa trypsin inhibitor and implication
A;Reference number: JH0607; MUID:92272755; PMID:1375466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hung, C.H.; Lee, M.C.; Lin, M.T.; Lin, J.Y.
ene 127, 215-219, 1993
;Title: Cloning and expression of the gene encoding Acacia confusa trypsin inhibitor th.
*Reference number: PN0539; MUID:93273234; PMID:8500764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title: The complete amino acid sequence of a Kunitz family trypsin inhibitor from seed; Reference number: JX0255; MUID:93224510; PMID:8468333
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: C72867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Cross-references: UNIPROT: P24924, GB: M92852, NID: g166233, PIDN: AAA32618.1, PID: g166234, Experimental source: seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: plant Kunitz-type proteinase inhibitor
C;Superfamily: secine proteinase inhibitor
C;Keywords: seed; serine proteinase inhibitor
C;T-136/Product: trypsin inhibitor (Kunitz) A chain #status experimental <MAT>
F;138-176/Product: trypsin inhibitor (Kunitz) B chain #status experimental <MAI>F;64/Inhibitory site: Lys (trypsin) #status predicted
F;133-142/Disulfide bonds: #status predicted
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:Residues: 1-176 <HU2>
;Cross-references: GB:M92852; NID:g166233; PIDN:AAA32618.1; PID:g166234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trypsin inhibitor (Kunitz) precursor - Acacia confusa
N;Contains: trypsin inhibitor A chain; trypsin inhibitor B chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                          A;Gene: Ac-p74
C;Superfamily: nuclear polyhedrosis virus p74 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42.5; DB 2;
Pred. No. 1.1e+02;
1; Mismatches 2;
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                               43.48;
71.48;
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Best Local Similarity 45.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 KLFNKN-PTLNDLG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KLYNKNSSTLKDLG 18
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A;Residues: 1-136;138-176 <WUH>
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu, H.C.; Lin, J.Y. Biochem. 113, 258-263, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-176 <HUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: JX0255
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                                                                                                                                                                                                                                                                                                                                                            RESULT 20
H70330
hypothetical protein aq 345 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: H70330
R;Deckert, G:; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUD:9819666; PMID:9537320
A;Accession: H70330
A;Accession: H70330
A;Accession: University; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-625 cAQP>
A;Cross-references: UNIPROT:O66676; GB:AE000685; NID:g2983026; PIDN:AAC06645.1; PID:g298
A;Cross-references: strain VF5
C;Genetics:
A;Gene: aq 345
C;Superfamily: uncharacterized conserved protein with VWA domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 21
WANNV74
WANNV74
WANNV74
WANNV74
C; Species: Autographa californica nuclear polyhedrosis virus
C; Species: Autographa californica nuclear polyhedrosis virus
C; Species: Autographa californica nuclear polyhedrosis virus
C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C; Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C; Accession: A; Faulkner, P.
Wirology 173, 759-763, 1989
Wirology 173, 759
Wirology 173
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C72867
C72867
C301
C5Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dsDNA virus
C;Date: 12.Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: C72867
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
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                                                                                                                                  Gaps
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                                                             2; Length 609;
                                                                                                                               6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                      Score 43; DB;
Pred. No. 89;
3; Mismatches
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Pred. No.
                                                                                                                                                                                                                                           273 DYKYYSDSIANFKDNGE 289
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KVFNENVYTLKDFSE 501
                                                          Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
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les 10; Conservative
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                                                                                                                                                                                                3 DYKLYNKNSSTLKDLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 KLFNKN-PTLNDLG 291
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Matches
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NiAlternate names: citrulline phosphorylase; ornithine transcarbamylase
CiSpecies: Bacillus subtilis
CiSpecies: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
CiAccession: Sil000; A38768; I40378; A65589; S38434
R;Mountain, A.; Smith, M.C.M.; Baumberg, S.
Moucleic Adids Res. 18, 4594, 1990
A;Title: Nucleotide sequence of the Bacillus subtilis argf gene encoding ornithine carba.
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A,Molecule type: DNA
A,Rosidues: 1-319 <MOU>
A,Crossereferences: UNIPROT:P18186; EMBL:X53360; NID:g39809; PIDN:CAA37444.1; PID:g39811
A,Accession: A38768
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A;Residues: 1, X', 3-14, XXX', 17-20, X', 22-30, XX', 33,'X', 35-39 <MOU2>
R;O'Reilly, M.; Devine, K.M.
Microbiology 140, 1023-1025, 1994
A;Title: Sequence and analysis of the citrulline biosynthetic operon argC-F from Bacillu A;Reference number: 140372; MUID:94297722; PMID:8025667
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A; Cross-references: EMBL: Z26919; NID:g408113; PIDN: CAA81542.1; PID:g408120
A; Cross-references: EMBL: Z26919; NID:g408113; PIDN: CAA81542.1; PID:g408120
C; Bron, S; Broullac, N; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Berter. C; Bron, S; Broullac, N.; Moszer, N.W.; Cho A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler. iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koothegtein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Y, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winterer, P.; Winterer, P.; Winterer, P.; Yamane, E.; Yoshida, K.; Yata, K.; Yoshida, K.; Ajttle: The complete genonce sequence of the Gram positive bacterium Bacillus subtilis.
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A;Experimental source: strain 168
                                                                                                      A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Reference number: A84930; MUD:20445173; PMID:10933077
A;Recession: F84951
A;Rotelminary
A;Molecule type: DNA
A;Residues: 1-292 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
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                                                   S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ornithine carbamoyltransferase (BC 2.1.3.3) - Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 2;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: yfjB; BU185
C;Superfamily: ATP-NAD/NADH kinase
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Best Local Similarity 47.1%;
Matches 8; Conservative
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                                                       l,Shigenobu, S.; Watana
Nature 407, 81-86, 2000
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Cispecies: Bacillus
Cispecies: Bacillus
Cispecies: Brood, Cispecies: Cispecie
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A;Reaidues: 1-262 <KUR>
A;Cross-references: UNIPROT:Q97WC9; GB:AE006641; NID:g13815601; PIDN:AAK42459.1; GSPDB:G
C;Genetics:
A;Gene: cbiF
C;Superfamily: Precorrin-4 C11-methyltransferase
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A,Cross-references: UNIPROT.032167; GB:Z99120; GB:AL009126; NID:g2635613; PIDN:CAB15262.
A,Experimental source: strain 168
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C;Accession: D90400
C;Accession: D90400
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Janzrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90400
A;Status: preliminary
A;Molecule type: DNA
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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
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Pred. No. 55;
1; Mismatches
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Pred. No. 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 42.9%;
Similarity 42.1%;
8; Conservative !
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87.5%;
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Best Local Similarity 87.5
Enes 7; Conservative
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SDYKMYNK 73
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ankyrin-like protein - Arabidopsis thaliana
NyAlternate names: protein F18022.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48596
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Les
Bubmitted to the Protein Sequence Database, April 2000
A;Reference number: 224493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deta-lactamase class C domain (PBPX family) containing protein [imported] - Clostridium . C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum (c)Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: B97245 F;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Recession: B97245 A;Accession: B97245 A;Accession: B97245 A;Accession: B97245
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A;Residues: 1-739 «KUR»
A;Cross-references: UNIRROT:097FD2; GB:AE001437; PIDN:AAK80752.1; PID:915025849; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
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Pred. No. 1.2e+02;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-591 «BEV.»
A;Cross references: UNIPROT: Q9LYA6; EMBL: DB
A;Experimental source: cultivar Columbia; BAC clone F18022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
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  240 SSLKLNNKDLLTLKOLG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 63.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 32/3; 7
A; Note: F18022.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 5
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A;Gene: CAC2808
                                                                                    RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable chromatin assembly factor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 0.1999 #sequence_revision 0.3-Dec-1999 #text_change 16-Aug-2004
C;Accession: T38471
R;Brown, D; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
sheference number: 221796
A;Reference number: 221796
A;Accession: T38471
A;Reference number: 221796
A;Accession: T38471
A;Reference number: 221796
A;Cession: T38471
A;Residues: 1-431 <-BRO-
A;Cession: T38471
A;Residues: 1-431 <-BRO-
A;Residues: 1-431 <-BRO-
A;Residues: 1-431 <-BRO-
A;Generics: strain 972h-; cosmid c29A4
C;Genetics:
A;Gene: SPDB:SPAC29A4.18
A;Map position: 1
A;Introns: 29/1; 64/2
C;Superfamily: WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scrinc/threonine-specific kinase (EC 2.7.1.-) isoform HST7-T - yeast (Candida albicans)
C;Species: Candida albicans
C;Species: Candida albicans
C;Date: Obsec-1996 #sequence_revision O6-Dec-1996 #text_change 16-Aug-2004
C;Date: O6-1996 #sequence_revision O6-Dec-1996 #text_change 16-Aug-2004
Mol-1996 #Secher Canstitutive activation Of the Saccharomyces cerevisiae mating response pathway
A;Reference number: S60154; MUID:96132546; PMID:8544826
A;Reference number: S60159
A;Molecule type: DNA
A;Residues: 1-589 cCLA>
A;Residues: 1-589 cCLA>
A;Resperimental source: isoform HST7-T
C;Superfamily: protein kinase homology
C;Reywords: AFP; phosphotransferase; protein kinase
F;247-564/Domain: protein kinase ATP-binding motif
                    A.Gene: argF
A.Map position: 100 (degrees)
A.Map position: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C.Superfamily: ornithine carbamoyltransferase
C.Keywords: arginine biosynthesis; transferase #status experimental <MAT>
F;1-319/Product: ornithine carbamoyltransferase #status experimental <MAT>
F;12-310/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
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                                                                                                                                                                                                                        Score 42; DB 1; Length 319;
Pred. No. 65;
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58.8%; Pred. No. 1.2e+02;
iive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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89;
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Pred. No. 89;
3; Mismatches
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 DYKLYNKNSSTLKDL 17
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EYKIWKKNSPFLYDL 43
                                                                                                                                                                                                                                                                                                                                          6 LYNKNSSTLKDLGE 19
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Matches 10; Conservative
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  C,Genetics:
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Length 591;

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Length 739; 2; Indels

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Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S. Sciance 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1035 «KUR»
A;Cross-references: UNIPROT:08UJX1; GB:AE008687; PIDN:AAL46042.1; PID:g17743801; GSPDB:G
A;Experimental source: strain C58 (Dupont)
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A;Cross-references: UNIPROT:P55937; EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BAA196
A;Experimental source: strain CD-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autotransporter protein bapA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
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R;Kondo, M.; Strou, S.
MAS Seq. 7, 71-82, 1997.
A;Title: Cloning and molecular characterization of CDNA encoding a mouse male-enhanced A;Reference number: Z22242; MUID:97217683; PMID:9063644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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                    Length 947;
               Score 42; DB 2; Length 947
Pred. No. 2.18+02;
3; Mismatches 3; Indels
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46.7%; Pred. No. 2.3e+02;
tive 5; Mismatches 3;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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               42.9%;
53.8%;
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267 DYGVYSRNASSATDL 281
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                                                                                                                                                                                                                                                                             287 YNKNNNNIDDLSE 299
               Query Match
Best Local Similarity 53.83
Matches 7; Conservative
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Matches 7; Conserv
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A; Molecule type: mRNA
A; Residues: 1-785 <07T3-
A; Experimental source: adult testis; clone DKRZp434A028
A; Experimental source: adult testis; clone DKRZp434A028
B; Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
B; Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
A; Reference number: Z18723
A; Reference number: Z18723
A; Accession: T17277
A; Accession: T17277
A; Residues: 569-785 <POU>
A; Residues: 569-785 <POU>
A; Residues: 569-785 <POU>
A; Cosserreferences: EMBL:ALI17503; NID:g5912010; PIDN:CAB55967.1; PID:g5912011
A; Experimental source: adult testis; clone DKFZp434E0635
A; Note: DKFZp434A028.1; DKFZp434E0635.1
C; Keywords: thiolester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein K12D9.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T2.5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25827
R;Graves, T.
R;
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A;Introns: 38/1; 122/1; 188/1; 209/1; 356/2; 374/1; 458/1; 524/1; 621/3; 746/1; 776/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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42.9%; Score 42; DB 2; Length 831;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2; Length 785;
Pred. No. 1.7e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain Bristol N2; clone K12D9 C; Genetics: A; Gene: CESP: K12D9.12
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A;Accession: T08605
A;Status: prellminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-947 <LOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| |: ||:| |::
456 SDYGLFIKNNSELNEI 471
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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675 KADYELYNKASN 686
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completed: November 24, 2004, 09:30:19 ne : 17.6957 secs
                                                     A; Molecule type: DNA
A; Residues: 1-615 <STO>
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A; Molecule type: mRNA
              A;Status: preliminary
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Matches
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B86212
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86212
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Huddes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
DNA segregation ATPase, FtsK/Spoilis family, YUKA B. subtilis ortholog [imported] - Cloe (;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: B97355
R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Residues: 1-1498 KUR>
A;Residues: 1-1498 KUR>
A;Residues: Clostridium acetobutylicum ATCC824
C;Genetics: A;Genetics: A,Genetics: A;Genetics: 
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NyAlternate names: ATPase 2
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Accession: 867483
R;Trottein, F.; Cowman, A.F.
Eur. J. Blochen. 227, 214-225, 1995
A;Tritle: Molecular cloning and sequence of two novel P-type adenosinetriphosphatases frc
A;Reference number: 867483; MUID:95154293; PMID:7851389
A;Accession: 867483
A;Accession: 867483
A;Accession: 867483
A;Kesidues: DNA
A;Residues: 1-1553 <TRO>
A;Residues: 1-1553 <TRO>
A;Residues: 1-1553 <TRO>
A;Introns: 17/2
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42.9%; Score 42; DB 2; Length 1553;
Best Local Similarity 42.1%; Pred. No. 3.5e+02;
Matches 8; Conservative 3; Mismatches 8; Indels
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A;Cross-references: UNIPROT:Q9LQP9; GB:AE005172; NID:g8439895; PIDN:AAF75081.1; GSPDB:GN:
Genetics:
A;Map position: 1
C;Superfamily: tomato leucine zipper-containing protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyaccession: W47555
R;Foldes, R.L.; Adams, S.L.; Fantaske, R.P.; Kamboj, R.K.
Biochim. Biophys. Acta 1223, 155-159, 1994
A;Title: Human N-methyl-D-aspartate receptor modulatory subunit hNR2A: cloning and seque: A;Reference number: S47555; MUID:94339179; PMID:8061049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1464 <FOL>
A;Cross-references: UNIPROT:Q12879; GB:U09002; NID:g558748; PIDN:AAB60343.1; PID:g558749
C;Superfamily: N-methyl-D-aspartate receptor 2A; glutamate receptor homology
F;428-854/Domain: glutamate receptor homology <GRH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-methyl-D-aspartate receptor modulatory chain hNR2A - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
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                                                                                                                                            Length 615;
                                                                                                                                                                                                   2; Indels
                                                                                                                                   42.3%; Score 41.5; DB 2;
illarity 55.6%; Pred. No. 1.6e+02;
Conservative 5; Mismatches 2;
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152 SDGELYSESSSELGKDIG 169
                                                                                                                                                                                                                                                           2 SDYKLYNKNSSTL-KDLG 18
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                                                                                                                                   Query Match
Best Local Similarity
Matches 10; Conserv
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                          OM protein - protein search, using sw model
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November 24, 2004, 09:11:04; Search time 101.152 Seconds (without alignments) 125.141 Million cell updates/sec Run on:

US-09-719-379A-2 Perfect score:

112 1 RSDYKLYNKNSSSNSTLKNLGE 22 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P43840 haemophilus	Q939pl lactococcus		-	Q82ca4 streptomyce	Q832y3 enterococcu													Q74br0 geobacter s	Aar35357 geobacter	Q8zjd9 yersinia pe	Aas60450 yersinia			Q61ex8 plasmodium	0	P59616 clostridium	-		2	Q8t357 plasmodium
SUMMARIES	αı	OM51 HAEIN	Q939 <u>₽</u> 1	TIG BUCAI	Q8STT1	Q82CA4	Q832Y3	Q8LL02	Q6L0G9	Q7RA98	Q7RL88	Q96Z64	Q6GUB7	Q9ALY8	Q7RF20	Q22762	Q8ILC9	Q7RHN4	Q9CUF6	Q74BR0	AAR35357	Q8ZJD9	AAS60450	QBMRNS	Q8T148	Q6LEX8	CAG25109	ARLY CLOTE	Q7RLW6	HRL2 LACMU	Q7K6A7	Q8T357
	DB		N	н	~	~	N	~	~	7	~	N	~	~	~	~	~	7	N	~	~	~	~	8	~	~	~	Н	~	Н	~	7
	Query Match Length	353	168	442	350	322	322	907	287	369	418	244	351	484	502	150	5561	245	384	409	409	106	706	952	1108	6761						229
di	Query Match	68.3	50.0	47.3	46.9	46.4	45.5	45.1	44.6	44.6	44.6	44.2	43.8	43.8	43.8	43.3	43.3	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.4	42.4	42.0	42.0	42.0
	Score	76.5	26	53	52.5	52	51	50.5	20	20	20	49.5	49	49	49	48.5	48.5	48	48	48	48	48	48	48	48	48	48	•	47.5	47	47	47
	Result No.	1	7	m	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23	24	25	26	27	28	29	30	31

Pfant, PF00621; OmpA; 1.
Pfant, PF00621; OmpA; 1.
Pfant, PF01389; OmpA membrane; 1.
PRINTS, PR01021; OMFADOWAIN.
ProDom; PD000930; OmpA/MotB; 1.
PROSITE; PS01068; OMPA; 1.

Q6dka7 xenopus lae O50827 borrelia bu	Q61273 methanococc Caf30312 methanoco	Q8w2n4 nicotiana t Q8dtd8 streptococc	Q756h9 ashbya goss Aas52963 ashbya go	Q7rcn2 plasmodium 003099 saccharomyc	Q6btm5 debaryomyce O7rf86 plasmodium		QB1d44 plasmodium
Q6DKA7 O50827	Q6LZ73 CAF30312	Q8W2N4 Q8DTD8	Q756H9 AAS52963	Q7RCN2 YMN3 YEAST	Q6BTMS O7RF86	Q868L5	Q8ID44
0 0	0 0	~ ~	~ ~	7 7	~ ~	~	8
246 308	426	510 842	606 606	1078	1612	1262	1262
42.0	42.0	42.0	42.0 42.0	42.0	42.0	41.5	41.5
47	47	47	47	447	47	46.5	46.5
32	34 35	36 37	8 6 6 6	4 4 1 4 1	4 4	44	4 2

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                           MEDLINE=95350630; Pubmed=7542800; Pickelses E.P., Relavede A. R., White O., Clayton R.A., Kirkness E.P., Pleischmann R.D., Addams M.D., White O., Clayton R.A., Marrick J.M., McKenney R., Bult. C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rd.";
Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-!- SIMILARITY: Belongs to the ompA family.
                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Outer membrane protein P5 precursor (OMP P5).
Names-omph, Synonyms-ompP5, OrderedLocusNames=HI1164;
Haemophilus influenzae.
353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006664; Bac OmpA.
InterPro; IPR002368; OmpA.
InterPro; IPR006665; OmpA/MotB.
InterPro; IPR006690; OMPA_LIKE.
InterPro; IPR006498; OmpA_Tmem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32796; AAC22819.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; C64187; C64187.
HSSP; P02934; 1QJP.
TIGR; HI1164; -
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=727;
HAEIN
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                              SIMILARITY: Belongs to the FKBP-type PPIase family. Tig subfamily.
                                                                                                                                                                                                                                                                                             HAMAP; MF_00303; -; 1.

InterPro: TRR001179; FKBP PPIAGE.

InterPro: IPR008880; Trigger_N.

InterPro: IPR008881; Trigger_N.

Pfam; PF006589; Trigger_C; 1.

Pfam; PF05697; Trigger_N; 1.

Pfam; PF05697; Trigger_N; 1.

Pfam; PF05697; Trigger_N; 1.

Pfam; PF05698; KMBP PPIASE; PALSE NEG.

Cell division; Complete proteome; Isomerage.

DOMAIN 16; 2488 PF1889; FKBP-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P., "Genome sequence and gene compaction of the eukaryote parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein ECU09_0790.

Name=ECU09_0790;

Encephalitozoon cuniculi.

Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.

NCBL_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; ALS90451; CAD27052.1; -.
GO; GO:0004114; F:3'.5'-yclic-nucleotide phosphodiesterase a.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR003607; Met_phos_hydro.
InterPro; IPR002073; PDEase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.3%; Score 53; DB 1; Length 442; 56.2%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 248 PPIase, FKBP-type.
442 AA; 53482 MW; FCC9950BF52150C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00233; PDEase I; 1.
SMART; SM0471; HDC; 1.
HPpochetical protein.
SEQUENCE 350 AA; 39803 MW; CE820F52979851B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 52.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21576510; PubMed=11719806;
                                                                                                                                                                                                                                                                         EMBL; AP001119; BAB13171.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 KLYNKNKNLKNTMKNI 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KLYNKNSSSNSTLKNL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 414:450-453(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
       similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GB-M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Name=tig; OrderedLocusNames=BU474;

Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).

Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-TOKYO 1998;
MEDLINE=20445173; PubMed=10993077; DOI=10.1038/35024074;
Middline=20445173; PubMed=10993077; DOI=10.1038/35024074;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
Nature 407:81-86(2000).
Involved in protein export. Acts as a chaperone by
maintaining the newly synthesized protein in an open conformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Lactococcus.
NCBI_TaxID=1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel RCR cryptic plasmid from
Complete protecome; Outer membrane; Porin; Signal; Transmembrane. SIGNAL 1 21 By similarity.
CHAIN 22 353 Outer membrane protein P5.
DISULFID 326 338 By similarity.
DOMAIN 272 316 OmpA-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
                                                                                                                                                                         68.3%; Score 76.5; DB 1; Length 353; 77.3%; Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 56; DB 2; Length 168; Best Local Similarity 73.3%; Pred. No. 3.6; Matches 11; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caccion and analysis of pBM02, a novel RCR cryptic pi Lactococcus lactis subsp cremoris P8-2-47.";
Plasmid 49:118-129(2003).
EMBL, AVO26767, AAK13013.1;
BYPOCHELICAL protein; Plasmid.
SEQUENCE 168 AA; 19397 MW; DB1B4221F94B2326 CRC64;
                                                                                                                         64ACB3E7BFF96B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                168 AA
                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                    132 RSDYKLYNENS---STLKKLGE 150
                                                                                                                                                                                                                                                                         1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22613826; PubMed=12726765;
                                                                                                                         37743 MW;
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                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanchez C., Mayo B.;
                                                                                                                         353 AA;
                                                                                                                                                                                                Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                DOMAIN
SEQUENCE
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                                                                                                                                                                         Query Match
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TIG_BUCAI
                                                                                                                                                                                                                      Matches
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Gaps

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Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R., Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis lyrata (Lyre-leaved rock-cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Natural selection for polymorphism in the disease resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 907;
                                                                                                                                     Fraser C.M., "Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22505406; PubMed=12618410;
Mauricio R., Stahl B.A., Korves T., Tian D., Kreitman M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
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                                                                                                                                                                                                                                                                                                                                                                         Complete protecome, Hypothetical protein.
SEQUENCE 322 AA; 37589 MW; 5E741BD49DCEA769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rp82 of Arabidopsis thaliana.";

Genetics 163:735-746 (2003).

BMBL, AP487796, AAM90858.1;

GO; GO:000524; F:ATP binding; IEA.

GO; GO:0000166; F:nuclectide binding; IEA.

GO; GO:000615; P:appptosis; IEA.

GO; GO:0042829; P:aefense response to pathogen; IEA.

InterPro; IPR00359; AAA ATPase.

InterPro; IPR000767; Disease_resist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.1%; Score 50.5; DB 2;
57.1%; Pred. No. 1.5e+02;
tive 4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.5%; Score 51; DB 2; Local Similarity 57.1%; Pred. No. 40; 12; Conservative 2; Mismathham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                907 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6L0G9;
05-JUL-2004 (TrEMBLrel. 27, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 RSDWKDYLYNVKSNNGTPSN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 ADYKLCNKVS---ATLKSIGE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYK--LYNKNSSSNSTLKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                              Enterococcus faecalis.";
Science 299:2071-2074(2003).
EMBL; AE016953; AAO81818.1; -.
TIGR; EF2085; -.
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SMART; SM00382; AAA; 1.
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InterPro; IPR002182; NB-ARC.
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nes 12; Conservative
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Pfam; PF00931; NB-ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Matches
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                        SKARRARA
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                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-WASS / ATCC 700802;
MEDLINE-V583 / ATCC 700802;
MEDLINE-22550857, Pubmed=12663927; DOI=10.1126/science.1080613;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seehadri R.,
Read T.D., Pouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
                                                            11;
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STRAIN-MA-4000 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NC11_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.4%; Score 52; DB 2; Length 322; Best Local Similarity 56.5%; Pred. No. 29; Matches 13; Conservative 3; Mismatches 5; Indels
                                                            Indels
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EMBL, AP005043; BAC73162.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 322 AA; 33126 MW; 2047P05D57BF7617 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                  263 DYRIFNKNSIAFWAEVYDDDDYNRTLENISE 293
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                                                                                                                                         3 DYKLYNKNSSS-----NSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                     322 AA
                ilarity 35.5%; Pred. No. 27;
Conservative 6; Mismatches
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(TrEMBLrel. 24, Last sequ
(TrEMBLrel. 24, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=SAV5450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
OrderedLocusNames=EF2085;
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                Best Local Similarity
Matches 11; Conserv
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01-JUN-2003
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01-JUN-2003
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082CA4,
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0832Y3
1D 0832
AC 0832
AC 0832
DT 01-J
DT 01-J
DE HYPC
GN 01-J
DE HYPC
GN 01-J
DE RYPC
GN COT
CO BAC
CO B
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092CA4
002CCA6
001-JU
01-JU
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Hypothetical protein.
SEQUENCE 369 AA; 43112 MW; 3651B52F57DD18AB CRC64;
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12368865;
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                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                                   Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C., Schepers B., Dock C., Antranikian G., Liebl W.; "Genome sequence of Picrophilus torridus and its implications for life
                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
-!- FUNCTION: Catalyzes the ferrous insertion into protoporphyrin IX
(By similarity).
-!- GATALYTIC ACTIVITY: Protoporphyrin + Fe(2+) = protoheme + 2 H(+).
-!- SIMILARITY: Belongs to the ferrochelatase family.
EMBL, AE017261; AAT43533.1; --
EMBL, AC017261; Fiferrochelatase activity; IEA.
InterPro; IPR001015; Ferrochelatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nature 419:512-519(2002).
-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Wan Lih L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardher M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                        Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Picrophilaceae; Picrophilus.
NCBI_TaxID=82076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 287; 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 AA; 33856 MW; 57773D59B089D554 CRC64;
                       Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom, PD002792; Ferrochelatase, 1.
Complete proteome; Heme blosynthesis; Iron; Lyase;
  (TrEMBLrel. 27, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00762; Ferrochelatase; 1.
                    05-JUL-2004 (TrEMBLrel. 27, La
Ferrochelatase (EC 4.99.1.1).
                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=DSM 9790 / ATCC 700027;
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                                                                OrderedLocusNames=PT00948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphyrin biosynthesis
SEQUENCE 287 AA: 338
                                                                                          Picrophilus torridus.
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                                                                                                                                                                                                                                              PubMed=15184674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=17XNL;
PubMed=12368865;
                                                                                                                                                                                                                                                                                                                                        around pH 0.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carucci D.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7RA98;
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shunway M.F., Bladbell S.L., Shallom S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasite Plasmodium yoelli yoelii.";
Nature 419:515-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                     Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 418;
                                                                     Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary data.

EMBL; AABLO1000732; BAA22135.1; -.
Hypothetical protein.
SEQUENCE 418 AA; 47948 WW; 7CC87D9D728DE1BC CRC64;
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
                        DB 2;
66;
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Pred. No. 76;
5; Mismatches
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                                                                                                                                                                                                                                                                                   418 AA
                                                                     5; Mismatches
                          Score 50;
                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 NNYNFFNKNSKINEYIKNI 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SDYKLYNKNSSSNSTLKNL 20
                        44.6%;
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                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                   8 NKNSSSNSTLKNLG 21
                                                                                                                                              |||::||:|
70 NKNNNSNNTIANIG 83
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                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium yoelii yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Query Match
Best Local Similarity
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Gaps

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"Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carlton J.W., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shalmon S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoalbi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                             Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Campylobacteraceae, Campylobacter.
NCBI_TaxID=197,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                               Length 484;
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47.6%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                 STRAIN=2523/90, Millar L.A., Ketley J.M.; Oldfield N.J., Millar L.A., Ketley J.M.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF314762, AAK08092.1; -. InterPro; IPR011029; DEATH_like. Hypothetical protein. SEQUENCE 484 AA; 57093 MW; 679216E902915034 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502 AA; 58790 MW; 51E90077E7BD30E9 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43.8%; Score 49; DB 2; I
66.7%; Pred. No. 1.2e+02;
tive 1; Mismatches 4;
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EMBL; AABLO1001514; EAA16830.1; -.
InterPro; IPR07201; Rrm_2.
Ema; PF04059; RRM 2; 1.
Hypothetical protein.
NON TER. 502 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 KAHNKNSSSKITFKN 218
                                                                                                                                                                                                                                                                                                                                                                                                                             5 KLYNKNSSSNSTLKN 19
                                                                                                                                                                                                                                                                                                                                    duery Match
Best Local Similarity 66.7%
Matches 10; Conservative
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Best Local Similarity
                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                    "Complete gandence of an aerobic thermoacidophilic crenarchaeon, Sulfolobus tokodaii strain?.";
DANA Res 8:123-140(2001).
EMBL; AP000988; BASA7062.1; -
GO, GO:0008757; F.S-adenosylmethionine-dependent methyltransf. . .; IEA. InterPro; IPR006542; FkbM.
InterPro; IPR006515; SAM bind.
TIGRFAM9; TIGR01444, fkbM fam; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 244 AA; 28182 MW; D19DCB1D4ABD9CF3 CRC64;
          Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
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                                                                                                                                                                                                                                                                                                                                                                                                          7;
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                                                                                                                                                                                                                                                                                                                                                             Query Match 44.2%; Score 49.5; DB 2; Length 244; Best Local Similarity 51.9%; Pred. No. 49; Matches 6; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Akridge H., Confer A. W., Dabo S. W.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-:-SIMILARITY: Belongs to the ompA family.
EMBL; AY643795; AAT55777.1; -.
InterPro; IPR006664; Bac_OmpA.
InterPro; IPR006665; OmpA/MotB.
R InterPro; IPR006669; OmpA_LIKE.
R InterPro; IPR006699; OmpA_LIKE.
R InterPro; IPR006699; OmpA_LIKE.
R PRINTS; PR01021; OmpA, I.
R PRINTS; PR01021; OmpA, membrane; 1.
R PRINTS; PR01022; OUTRWHBRANEA.
R PRODOM; DD00939; OmpA/MotB; 1.
R PRODOM; DD00939; OmpA/MotB; 1.
R PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%; Score 49; DB 2; Length 351; 55.6%; Pred. No. 87; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 SDYKDVVKNLSKNGYKIRVEHTLKNLG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SDYKLYNKNSSSNS-----TLKNLG 21
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01-JUN-2001 (TrEMBLrel. 17, Created)
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MEDLINE=21456156; PubMed=11572479;
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Matches 10; Conservative
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Q9ALY8
ID Q9ALYI
AC Q9ALYI
DT 01-JUJ
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Q6GUB7
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3 DYKLYNKNSSSNSTLKN 19
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hes 10; Conservative
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                                                                                                falciparum.
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07RHN4
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Q9CUF6
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MEDIJNE-22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angiudli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 150;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U41546; AAC48218.1; -.
PIR; T28904; T28904.
Wormhep; T25B6.3; CE05013.
Hypothetical protein.
SEQUENCE 150 AA; 17900 MW; F4B29447B9F8FA4D CRC64;
                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein T25B6.3.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.3%; Score 48.5; D
46.2%; Pred. No. 40;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 OSDHHLYNKYFFHLGHNFLSNCTVKN 115
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MEDLINE-99069613; PubMed-9851916;
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
Hypothetical protein.
ORFNames=PF14_0315,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 46.2
hes 12; Conservative
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
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Matches
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0811C9
081C0
DD Q81LC
DD Q81LC
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DT 01-MA
DD O1-MA
DD ON-MA
DD ON-M
RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                          Nature 419:498-511 (2002).

EMBL; AE014821; AAN36928.1; -..

EGO; CO:000357; F:DNA binding; IEA.

GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.

INTER-Pro; IPR01965; Znf_PHD.

SMART; SM00249; PHD; 4.
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.; Meman malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  43.3%; Score 48.5; DB 2; Length 5561; 33.3%; Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium yoelli yoelli.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                        5561 AA; 658527 MW; 98BF06CAC3C2B52B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
1-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 48; DB 2;
52.9%; Pred. No. 82;
tive 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
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EMBL; AABLO1001178; EAA15745.1; -.
Hypothetical protein.
NON TER 245 245
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Hypothetical protein.
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STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/61; TISSUE-Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB-Testis;
Adachi J., Alzawa K., Akahira S., Pukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kosukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Muramatsu M., Hayashizaki Y.,
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last sequence update)
010-MAR-2004 (TrEMBLrel. 26, Last convertion update)
010-MAR-2004 (TrEMBLrel. 26, Last convertion update)
11 musculus adult male testis convertion (Trempt enriched library, clone:4930577N17 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PETRAIN=CSTBL/61; TISSUE=Testis;

MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matumoto H., Sakaguchi S., Ikegami T., Rashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integarated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-GSTBL/60, TISSUE-Testis;
MEDLINE-2108560; Debed-11217851;
RIKER FANYOM CONSORtium;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL, MAC16297; BAB30183.1; -.
                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                            sequence. (Fragment).
Name=4930577N17Rik;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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MGD; MGI:1914996; 4930577N17Rik.

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PubMed=14671304; DOI=10.1126/science.1088727;
Mathe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Madupu R., Brinkac L.M., Daugherty S.C., DeBOy R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.
Weidman J.F., Khouri H.M., Fraser C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                             Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
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Geobacteraceae; Geobacter.
NCBI_TaxID=35554;
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                                      Score 48; DB 2; Length 384
Pred. No. 1.4e+02;
1; Mismatches 6; Indels
SEQUENCE. 384 AA; 41209 MW; E9856EA599F28262 CRC64;
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SEQUENCE 409 AA; 46361 MW; 27EABC4A3A7D6BEF CRC64;
                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, La
Hypothetical protein.
ORFNames=GSU1981;
Geobacter ...
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EMBL; AE017180; AAR35357.1; -.
TIGR; GSU1981; -.
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                                                                                                                                                   347 YATYNQFSRKNCTLKNL 363
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                                      42.9%;
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27,
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DYRYYARNSRSDDTTHNL
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                                    Query Match
Best Local Similarity 58.8
Matches 10; Conservative
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                                                                                                                                                                                                                                               PRELIMINARY;
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STRAIN=PCA / ATCC 51573;
PubMed=14671304;
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02-MAR-2004 (TrEMBLrel.
02-MAR-2004 (TrEMBLrel.
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SEQUENCE FROM N.A.
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AAS60450;
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QBMRN5
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AAS60450
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STRAIN=91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=1242430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonouph K.A., Nilles M.L., Matson J.S., Blattner F.R.,
Perry R.D.;
Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.; "Genome of Geobacter sulfurreducens: metal reduction in subsurface environments.";
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MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Parkhill J., Wasalahia M., Edwas K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Feltwell T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.9%; Score 48; DB 2; Length 409; 50.0%; Pred. No. 1.5e+02; ive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBZJD9; Q74Y13; Q7CFV4; 01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OT-2004 (TrEMBLrel. 28, Last annotation update) Putative membrane protein (Hypotheital protein y3955). OrderedLocusNames=YP0173, YP00174, Y3955;
                                                                                                                                                                                                                                                                                                                                                        11 protein.
409 AA; 46361 MW; 27EABC4A3A7D6BEF CRC64;
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J. Bacteriol, 184:4601-4611(2002).
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InterPro; IPR010289; DUF893.
InterPro; IPR009058; Wing_hix_DNA_bnd.
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EMBL; AE017214; AAR35357.1; -.
TIGR; GSU1981; -.
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79 DYRYYARNSRSDDTTHNL 96
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Best Local Similarity 50.01
Fig. 20 Processive
Fig. 20 Processive
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082J09
082J09
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STRAIN-91001 / Biovar Mediaevalis;
SOND Y., TONG Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou I SOND Y., TONG Z., Wang L., Han Y., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R.;
Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017127; AAS60450.1; --
SEQUENCE 706 AA; 79672 MW; 6313A6E7DDFC07FD CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
6H1246pp (GG312133-Ph).
Name=CG5839; ORFNames=CG31233;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroides Drosophilidae; Drosophila.
                                                                                                                                                                        42.9%; Score 48; DB 2; Length 706; 40.0%; Pred. No. 2.7e+02; ive 6; Mismatches 6; Indels
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40.0%; Pred. No. 2.7e+02;
ative 6; Mismatches 6; Indels
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[2]
InterPro, IPR010020; YCCS_YHJK.
Pfam; PF05976; DUF893; 1.
TIGRPHAG; TIGR01667; YCCS_YHJK; 1.
Complete Proteome; Hypothetical protein.
SEQUENCE 706 AA; 79672 MW; 6313A6E7D0FC07FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAR-2004 (TrEMBLrel. 27, Created)
24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Putative membrane protein.
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NCBI_TaxID=632;
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Matches 8; Conservative
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SEQUENCE FROM N.A.
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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                           RA MEDINE-2019000; Unbec=10/31131;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Radion R.C., Rogers Y.H., Blazej R.G., Champe M., Ffeiffer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Champe M., Ffeiffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Baytaktaroglu L., Belahako S.M.,

Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Brotter P., Brotter B.M.,

Burtis R.C., Busem D.A., Buller H., Cadieu E., Center A., Chan'r

RA Burtis R.C., Busem D.A., Buller H., Cadieu E., Center A., Chan'r

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Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Burtis N.C., Evangelista C.C., Ferraz C., Ferriar B.M., Glasser K.,

RA Hortin D., Houston K.A., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Helman T.J., Wel M.H., Ibeywan C.,

Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Hostin D., Houston K.A., Meland T.J., Wel M.H., Ibeywan C.,

Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.,

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Murany D.M., Nelson D.L.,

Ralasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Ralasco D.M., Pittman G.S., Pan S., Pollard J., Puri V., Reangon D.,

Reinert K., Reinington K.A., Nixon K., Nussekern D.R., Pacleb J.M.,

Spier E., Spradling A.C., Stapleton M., Stupski M., San B.,

Spier E., Spradling A.C., Stapleton M., Stupski M., San B.,

Steinex E., Spradling A.C., Stapleton M., Stupski M., San B.,

Reinbar R.M., Woden B.M., Weinstock G.M., Weissenbach J.,

When B.C., Siden-Kamos I. Stapleton W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-2242065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Ffeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RSSEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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MEDLINE=22426070; PubMed=12537573;
                   MEDLINE=20196006; PubMed=10731132;
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systematic review.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN'2002 (TrEMBLrel. 21, Created)
01-JUN'2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Homeobox-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                             GO; GO:000419; P:membrane alanyl aminopeptidase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPror; IFRO01930; Peptidase_M1.
Pfam; PF01433; Peptidase_M1, 1.
PRINTS; PR00756; ALADIPTĀSE.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 952;
                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 48; DB 2; Length 952
45.0%; Pred. No. 3.76+02;
Virmarrhes 7; Indele
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                                                                                                                                Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                      to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                    952 AA; 106857 MW; A42AB7D83C78812C CRC64;
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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GO; GO:0005634; C:nucleus; IEA.
Nuclear protein.
SEQUENCE 1108 AA; 124003 MW;
                                                                                                                                                                                                                            FlyBase; FBgn0051233; CG31233
                                                                                                                                                      EMBL; AY119508; AAM50162.1;
EMBL; AE003736; AAF55912.3;
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nes 9; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 418:79-85(2002).
                                         Submitted (SEP-2002)
                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
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Q8T148;
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Q6LEX8;
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STRAIN=3D7
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"Sequence of Plasmodium falciparum chromosomes I, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
A Drmond D., Sanders M., Hayes K., Hall S., Quail M., Barrell B.G;
Us bubitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

IN EMBL, CR38401; CAG25109.1; -.
RMIL, CR38401; CAG25109.1; -.
RMILCEPTC; IPRO01480; Bromodomain.
RITCEPTC; IPRO01480; Br Hand like.
RITCEPTC; IPRO10983; EF Hand like.
RITCEPTC; IPRO10981; EF Hand like.
RITCEPTC; IPRO114965; Caf FHD.
RITCEPTC; IPRO0144; SPT.
RITCEPTC; IPRO014965; Zaf FHD.
REAM: PPO0499; Bromodomain; 1.
REAM: PPO0659; PHD; 1.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative SET-domain protein (Set-domain protein, putative).
ORFNames-MAL6P1.131, PFF1440w;
Plasmodium falciparum (isolate 3D7).
Eukarryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.9%; Score 48; DB 2; Length 6761; 36.4%; Pred. No. 3.2e+03; ive 8; Mismatches 6; Indels
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PROSITE; PS50014; BROMODOMAIN 2; 1.
PROSITE; PS502080; SET; 1.
PROSITE; PS502080; SET; 1.
PROSITE; PS5020159; ZF PHD 1.
PROSITE; PS50016; ZF PHD 2; 1.
SEQUENCE 6761 AA; 797029 WW; 6FD6CA835134F303 CRC64;
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Last annotation update)
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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SMART; SM00249; PHD; 4.
SMART; SM00317; SET; 1.
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Matches 8; Conservative
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                                                                                                                          SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=36329;
                                                                                                                                         PubMed=12368867;
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14-APR-2004
14-APR-2004
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CAG25109;
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CAG25109
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Mungall K., Bewman S., Atkin R., Baker S., Barron A., Brooke K., Amingall K., Bowman S., Atkin R., Baker S., Barron A., Brooke K., Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Cherevach I., Chillingworth C., Christodoulou Z., Clark L., Clark B., Corto C., Croin A., Davies R., Davies P., Dear P., Dearden F., Doggett J., Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z., Hamptray S., Jagels K., James D., Johnson D., Lennard N., Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L., Oliver K., Normond D., Price C., Quail M.A., Rabbinowitsch E., Rajandream M.-A., Rutter S., Rutherford K.M., Sanders M., Simmonds M., Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K., Taylor K., Tivey A., Unwin L., Whitchead S., Woodward J., Sulston J.E., Craig A., Redponter O. Plasmodlum falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=3D7;
Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J.,
Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G;
Submitted (WAR-2004) to the EWBL/GenBank/DDBJ databases.
EMBL; CR384401; CAG25109 JI, CAG25109 MW; 6FD6CA835134F303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
-1- CATALYTIC ACTIVITY: N-(L-arginino) succinate = fumarate + L-
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MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
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Clostridium tetani.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
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10-0CT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Argininosuccinate lyase (BC 4.3.2.1) (Arginosuccinase) (ASAL)
                               MAL6P1.131.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium; Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6761;
Putative SET-domain protein (SET-domain protein, putative)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.9%; Score 48; DB 2; I 36.4%; Pred. No. 3.2e+03; tive 8; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                   MCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                      PubMed=12368867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARLY_CLOTE
ID ARLY_CLOTE
AC P59616;
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57.9%; Pred. No. 2.6e+02;

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Local Similarity 57.9
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                   LACMU
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Q7K6A7.
ID Q7K6A7
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Best Loca
Matches
                                                                                                                                                                                                                                                                               RESULT 29
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                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstands. Let be between the Swiss Institute of Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ï
   SIMILARITY: Belongs to the lyase 1 family. Argininosuccinate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carlton J.W., Adgiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Eradlaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Carucci D.J., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
42.4%; Score 47.5; DB 1; Length 438;
Best Local Similarity 41.4%; Pred. No. 1.9e+02;
Matches 12; Conservative 3; Mismatches 5; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmodium yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; AABL01000665; EAA21865.1; -.
GO:0003899; F:DNA-directed RNA polymerase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-directed RNA polymerase.
enrimenre 595 AA; 71812 MW; 0C546431C87F5663 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0838; argH; 1.
PROSITE; PS001.63; FUMARATE LYARES; 1.
Arginine biosynthesis; Complete Procteome; Lyase.
SEQUENCE 438 AA; 50296 WW; 97CCEDIEZ7807C53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 DYKLYNKNSS-----SNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAE, MF 00006; -; 1.
InterPro; IPR003049; argH.
InterPro; IPR003031; D Crystallin.
InterPro; IPR00362; Pumarate lyase.
InterPro; IPR008948; L-Aspartase-like.
PRIMTS; PR00145; DCRXSTALLIN.
PRINTS; PR00149; FUMRATELYASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Crea
01-MAR-2004 (TrEMBLrel. 26, Last
01-MAR-2004 (TrEMBLrel. 26, Last
DNA-directed RNA polymerase III.
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE015937; AA035181.1; -. HSSP; P24058; 1DCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=73239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=PY02422;
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42.4%; Score 47.5; DB 2; Length 595;

Query Match

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MEDLINE=91224327; PubMed=2026257;
Sanchez E.F., Diniz C.R., Richardson M.;
Sanchez E.F., Diniz C.R., Requence of the haemorrhagic factor LHFII, a mttalloproteinase isolated from the venom of the bushmaster snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ninterPro; interPro; Peptidase M12B.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR006025; Pept M Zn_BS.
Pfam; PF0421; Reproclysin; I.
PROSITE; PS00142; ADAM MEPRO; I.
PROSITE; PS00142; ZINC_PROTEASE; I.
Calcium-binding; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Zinc.
7 Calcium (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Lachesis muta muta).";
FEBS Lett. 282:178-182(1991).
-!- FUNCTION: This protein is a zinc protease from snake venom that
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Lachesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium (By similarity).
Calcium (By similarity).
Calcium (By similarity).
By similarity.
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Calcium (By similarity).
Calcium (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acts in hemorrhage.
-!- COFACTOR: Binds 1 zinc ion and 2 calcium ions per subunit.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to peptidase family M12B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.0%; Score 47; DB 1; Length 200; 47.6%; Pred. No. 92;
     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934954B56785DB13 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Moorrhagic factor II (BC 3.4.24.-) (LHF-II). Lachesis muta muta (Bushmaster).
                                                                                                                                                                                                                                  200 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 AA
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclin2 related protein, putative. Name=PFE0920c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNODLINVOSAANDTLKTFGE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SDYKLYNKNSSSNSTLKNLGE 22
                                                                                   : || | | || || || || 456 KKDYYL-NKNSNYNNILKN 473
                                              1 RSDYKLYNKNSSSNSTLKN 19
                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22596 MW;
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Matches 10; Conservative
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                                                                                                                                                                                                                                STANDARD;
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Best Loc
Matches
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                                                                                                        MEDLINE=2225708; PubMed=1236867;
MEDLINE=2225708; PubMed=12368867;
Mall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherwach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
Cronin A., Davies R., Dear P., Dearden F., Deggett J.,
Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
Harper D., Haueer H., Hornsby T., Holroyd S., Horrocks P.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
Sulston J. E., Craig A., Newbold C., Barrell B.G;
M. Schenon C. E plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A., Hall N., Bowman S., Churcher C., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DbBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 42.0%; Score 47; DB 2; Length 229; Local Similarity 52.9%; Pred. No. 1.18+02; Nes 9; Conservative 3; Mismatches 5; Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 AA; 26846 MW; D34490978209D930 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 229 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 278:39839-39850(2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL929353; CAD51548.1; -. InterPro; IPR011028; Cyclin like. InterPro; IPR006671; Cyclin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSDYKLYNKNSSSNSTL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00134; Cyclin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 419:527-531(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Putative cyclin 3.
Name=cyc-3;
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q8T357;
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A KEDLINE=22388257; PubMed=12477932;

A KINSUGENPY

A KLUSOGENPY

A Lidusner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lidusner R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Lidtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Muzny D.W., Gareen B.D., Dickson M.C.,

B Hakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

A Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                  Length 229;
                                                                                                                                                                                                                                                                               / Match 42.0%; Score 47; DB 2; Length 229
Local Similarity 52.9%; Pred. No. 1.1e+02;
nes 9; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Strausberg R., Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC074453; AAH74453.1; -. Hypothetical protein.
                                                                                                                                                                                                              229 AA; 26846 MW; D34490978209D930 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 AA; 27636 MW; B67B0E0988C2E1A7 CRC64;
-1- SIMILARITY: Belongs to the cyclin family. EMBL, A4416697; CAC95051.1; ... InterPro; IPR011028; Cyclin like. InterPro; IPR006671; Cyclin N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSDYKLYNKNSSSNSTL 17
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                                                                                                                                             Pfam; PF00134; Cyclin_N; 1.
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                                                                                                                                                                             Cyclin.
SEQUENCE
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SEOUENCE
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Q6DKA7;
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Length 426;

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Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
                                                                                                                                             "Complete genome sequence of the mesophilic hydrogenotrophic methanogen Methanococcus maripaludis.";
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BX957221; CAF30312.1; CCMplete proteone; Hypothetical protein.
SEQUENCE 426 AA; 50079 MW; 2E07C24D217F6AC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%
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Matches 11; Conservative
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                                                                                                                         Leigh J.A.;
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CAF30312;
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Q8W2N4
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STRAINS-ATCC 35210 / B31;
STRAINS-ATCC 35210 / B31;
STRAINS-ATCC 35210 / B31;
Fraser C.M., Casjens S., Hubmed-9403685; DOI=10.1038/37551;
Fraser C.M., Casjens S., Hubmed-9403685; Doi-10.1038/37551;
Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
Richardson D.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
Gocayne J.D., Weidman J.F., Utterback T.R., Watthey L., McDonald L.A.,
Artiach P., Bowman C., Garland S.A., Fujil C., Cotton M.D., Horst K.,
Roberts K.M., Hatch B., Sailth H.O., Venter J.C.;
Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Handrickson B.L.; Kaul R., Zhou Y., Bovee D., Chapman P., Chung J., Conway de Macario E., Dodsworth J., Gillett W., Graham D.B., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia.
NCBI_TaxID=139;
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                                        Length 246;
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                                                                                                                    4; Indels
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Pfam; PF02414; Borrelia_orfA; 1.
Complete protecome; Hypothemical protein; Plasmid.
SEQUENCE 308 AA; 36494 MW; E8233C4660C5A015 CRC64;
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Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanococcaceae; Methanococcus.
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Last annotation update)
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Last annotation update)
                                42.0%; Score 47; DB 2; I
56.2%; Pred. No. 1.2e+02;
iive 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Lyme disease spirochete)
Plasmid 1p36.
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EMBL; AE000788; AAC66174.1; -.
PIR; A70254; A70254.
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                                                                                                                                                                                                                                     81 YNSNSSSSTTTQNRAE 96
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183 IYNKNSIENSFLKKI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein BBK23.
OrderedLocusNames=BBK23;
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OrderedLocusNames=MMP0756;
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                                                                                                                    Conservative
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Query Match
Best Local Similarity
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1050827
10 050827
AC 050822
AC 050822
AC 050822
AC 05082
BD 01-JU
DT 01-JU
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061273
10 061273
AC 06127
DT 05-JU
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Nicotiana.
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S2 / LL;
Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
Saenphimmachak C., Soell D., Whitman W.B., Larimer F.W., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the mesophilic hydrogenotrophic methanogen Methanococcus maripaludis.", Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BX957221; CAF30312.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.0%; Score 47; DB 2; Length 426; 50.0%; Pred. No. 2.1e+02;
                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 426 AA; 50079 MW; 2E07C24D217F6AC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea, Buryarchaeota, Methanococci, Methanococcales,
Methanococcaceae, Methanococcus.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome P450-dependent fatty acid hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
42.0%; Score 47; DB 2; 1
50.0%; Pred. No. 2.1e+02;
tive 2; Mismatches 9
                                                                                                                                                                                                                                                                                                                           426 AA.
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                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                   1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSDYKLYNKNSSSNSTLKNLGE 22
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326 KSDKKKTNKKIGTNSILKNM 345
                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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762 YEYYNKNGAPNSTV 775
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Best Local Similarity 57.22
Best Local 8; Conservative
                                                                                             PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=ATCC 10895;
PubMed=15001715;
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PubMed=15001715;
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                                                                                                                                                                                                                                             NCBI_TaxID=33169;
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                                                                                                                                                                      AER282Wp.
Name=AER282W;
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                                                                                                           2756H9;
                                                                                           Q756H9
                                                              RESULT 38
Q756H9
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R GO; GO:000524; F:ATP binding; IEA.

R GO; GO:0001602; C:membrane; IEA.

R GO; GO:000166; F:nucleotide binding; IEA.

R GO; GO:0001810; P:transport; IEA.

R GO; GO:0001810; P:transport; IEA.

R GO; GO:0001810; P:transport; IEA.

R TherPro; IPR003593; AAA ATPase.

R TherPro; IPR003593; DuT214.

R Féam; PF00005; ABC_transporter; 1.

R Féam; PF000006; ABC_transporter; 1.

R From, PF000006; AAA; 1.

R PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

R PROSITE; PS00211; ABC_TRANSPORTER_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ABC transporter, membrane protein subunit and ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=UAIS9 / ATCC 700610 / Serotype c;
STRAIN=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
Adid D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
Qian Y., Li S., Zhu H., Najar P.Z., Lai H., White J., Roe B.A.,
Ferretti J.J.;
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                                                                                                                                                                                                              42.0%; Score 47; DB 2; Length 510; ilarity 36.8%; Pred. No. 2.6e+02; Conservative 9; Mismatches 3; Indels
   LeBouquin R., Kahn R., Benveniste I., Durst F.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Complete proteome. 842 AA; 93216 MW; EFF8E211B756228F CRC64;
                                                                                                                                                                      Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 510 AA; 58633 MW; 67F0FD6472DAA182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
-!- SIMILARITY: Belongs to the ABC transporter family.
BED: AE014974; AANS9077.1; --
HSSP; QS8206; 1L2T.
                                             EMBL; AF092913; AAL54884.1; -. GO: 0004497; F: monooxygenase activity; IEA. GO; GO: 0006118; P: menooxygenase activity; IEA. INTERPRO; GO: 0006118; P: electron transport; IEA. INTERPRO; IPR001128; Cytochrome P450. InterPro; IPR002401; EP4501. PF8001; PF00067; P450; 1. PRINTS; PR00463; EP4501. PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                 842 AA
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                                                                                                                                                                                                                                                                                            103 KTNFQVYQKGHNSNTTLKD 121
                                                                                                                                                                                                                                                                           1 RSDYKLYNKNSSSNSTLKN 19
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Best Local Similarity 50.04
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Matches 7; Conserv
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Q8DTD8
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1 RSDYKLYNKNSSSNSTLKNL 20

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"The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
Science 304:304-307(2004).
Science 304:304-307(2004).
SEMBL, ARS120631.
                                                                                                                                                                                                                                                                                                                                                                                                                     Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S., Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A., Gaffney T.D., Philippsen P.;
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                                                                                                                                                                                       Ashbya gossypii (Yeast) (Eremothecium gossypii).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Eremothecium.
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Bukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Bremothecium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Ashbya gossypil genome as a tool for mapping the ancient Saccharomyces cerevialae genome.";
Science 304:304-307(2004)
EMBL; AE016897; AAS52963.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.0%; Score 47; DB 2; Length 909; 57.1%; Pred. No. 4.9e+02; ive 3; Mismatches 3; Indels
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57.1%; Pred. No. 4.9e+02;
tive 3; Mismatches 3; Indels
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Pfam; PF02714; DUF221; 1.
SEQUENCE 909 AA; 102992 MW; 9D95C4EC70B98293 CRC64;
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23-APR-2004 (TrEMBLrel. 27, Last sequence update)
23-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                              Last annotation update)
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909 AA.
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                                                       Created)
  PRT;
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Best Local Similarity 57.1.
Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AABLO1001863; EAA17814.1; -.
GO; GO:00301319; C:clathrin coat of trans-Golgi network vesicle; IEA.
GO; GO:000301319; C:clathrin coat of trans-Golgi network vesicle; IEA.
GO; GO:0006461; P:protein complex assembly; IEA.
InterPro; IFR008152; A/G adapt C.
InterPro; IFR008153; Adaptin N.
Pfam; PF01602; Adaptin N.
Probom; PF02183; Alpha adaptin C.
Probom; PF0218457; Gamma adaptin C; 1.
PROSITE; PSS0180; GAE; II.
SEQUENCE 1078 AA; 122919 FW; 6AC61A9B32CC649B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parasite Plasmodium yoelli yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó,
                                                                                                                                                                                                                 Plasmodium yoelli yoelli.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.0%; Score 47; DB 2; Length 1078; larity 62.5%; Pred. No. 5.9e+02; Conservative 1; Mismatches 5; Indels
                                                                                                                                               01-MAR-2004 (TrEMBLrel. 26, Last sequence update) Adapter-related protein complex 1 gamma 1 subunit.
                                                                                                        PRT; 1078 AA.
                                                                                                                                          Created)
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|: |||| : |||:
762 YEYYNKNGAPNSTV 775
                                                                                                                                        (TrEMBLrel. 26,
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 PubMed=12368865;
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                                                                                                                                          01-MAR-2004
                                                                  RESULT 40
Q7RCN2
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Db 622 LYNKNSGSNRSFGVLG 637
Search completed: November 24, 2004, 09:28:53
Job time: 105.152 secs

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; Search time 82.8152 Seconds (without alignments) 82.302 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                         November 24, 2004, 09:07:49
                                                                       - protein search, using sw model
                                                                                                                                                                                                                   1 RSDYKLYNKNSSTLKDLGE 19
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Gapop 10.0 , Gapext 0.5
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98
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length: 0 length: 2000000000 sed sed 88 Minimum I Maximum I

Total number of hits satisfying chosen parameters:

2002273 segs, 358729299 residues

Searched:

2002273

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* A_Geneseq_23Sep04:* geneseqp20048:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1		Aay79990 Non-typea		Aab47442 LB1(f) co	Aab47446 Entire 3r	Abg80420 Haemophil			Aay79977 Non-typea					Aab47440 LB1(f) co		Aay79993 Plasmid L	Aay79980 Non-typea			Aaw98915 ISER prot	Aaw98914 IER prote	Aar80132 Rps2 dise	Aar83440 A.thalian		Abul7574 Protein e
SUMMARIES	a	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AAY79978	AAY79990	AAY79984	AAB47442	AAB47446	ABG80420	AAY79979	AAB47447	AAY79977	AAY79975	AAY79988	AAY79983	AAY79974	AAB47440	AAB47444	AAY79993	AAY79980	AAY79976	AAW98912	AAW98915	AAW98914	AAR80132	AAR83440	AAW98913	ABU17574
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de	Query		100.0	100.0	100.0	100.0	100.0	100.0	89.3	88.8	83.7	83.7	83.2	83.2	83.2	83.2	83.2	83.2	77.0	76.5	50.0	50.0	50.0	50.0	50.0	50.0	49.0
	Score		98	96	96	96	96	96	87.5	87	82	82	81.5	81.5	81.5	81.5	81.5	81.5	75.5	75	49	49	49	49	49	49	48
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ABU17880 ABB61039 ABU24397 ABU24323 ADNS9952 ADNS9952 ADNS99504 ABP27295 ADN73899 ADN4312 ADK4379 ADK4379 ADK4379 ADK52869 AAM50854 ABR52727 ABR52727	ADK62734 AAY79962 ADN63374
536 6 200 4 200 4 1829 8 1143 4 1143 4 1143 6 1017 8 1017 8 1017 8 1017 8 1018 6	1216 7 1216 7 19 3 58 8
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ALIGNMENTS

Vaccine, non-typeable Haemophilus influenzae, ntHi; infection, chimeric protein, Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f), immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection. Non-typeable H. influenzae group 2 LB1(f) peptide N1236MEE. × (SMIK) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS) UNIV OHIO STATE RES FOUND. AAY79978 standard; peptide; 19 AA 98GB-00012613. 99WO-US011980. (first entry) Haemophilus influenzae 28-MAY-1999; 11-JUN-1998; WO9964067-A2 15-MAY-2000 16-DEC-1999 AAY79978;

Lobet Dequesne G, Bakaletz LO, Cohen J,

WPI; 2000-116457/10.

Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.

Example 1; Page 30; 68pp; English

The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis; or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. influenzae and probes from the present invention can be used for diagnosis of H. influenzae infection. AAX79955 to AAX79933, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention

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AAY79990;

RESULT 2

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us-09-719-379a-4.rag

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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAX71955 to AAX7993, and AAX91201 to AAX91252, represent sequences used in the exemplification of the present invention
                                                                                                                                Vaccine, non-typeable Haemophilus influenzae, ntHi; infection, chimeric protein, Haemophilus influenzae, P5-like fimbrin protein, lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope; ottiis media; sinustiis; conjunctivitis; looper respiratory tract infection.
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                                                                                              Non-typeable H. influenzae group 2b LB1(f) peptide NTHI-183.
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100.0%; Pred. No. 1.5e-09;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
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                                                         15-MAY-2000 (first entry)
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                       Haemophilus influenzae.
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                    AAY79984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes antigenic P5-like fimbrin subunit peptides (LBI(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAX79933, and AAS91201 to AAA291252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Hamphilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(E); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                            Non-typeable H. influenzae 183NP Group 2b type peptide.
                                    100.0%; Score 98; DB 3; I 100.0%; Pred. No. 1.5e-09;
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100.0%; Pred. No. 1.5e-09;
ive 0; Mismatches 0;
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                                                                                                                                           1 RSDYKLYNKNSSTLKDLGE 19
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae
                    Query Match
Best Local Similarity
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Sequence 19 AA;
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AAY79990

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AAY79984 ID AAY

RESULT 3

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15-AUG-2002
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                                                                                                                                                                                                                            The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein PS; (MOMP PS) of non-typeable H. influenzae (htHi). Each of these peptides contain an LBI(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP PS from strain ntHill138, representing amino acids Argl17 to Gly135. This peptide represents the third exposed loop of PS and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Haemophilus
                                                                                                                                                   Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface exposed loop; major outer membrane protein P5; MOMP P5;
non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
ottis media; sinusitis; conjunctivitis;
lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                          influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Entire 3rd loop from strain ntHi-183NP (Group 2b type).
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                                                                                                          Thonnard J;
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                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                                          Poolman J,
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                                                                                                                                                                                                           Claim 1; Page 26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RSDYKLYNKNSSTLKDLGE 19
                                           13-FEB-2001; 2001WO-EP001556
                                                               15-FEB-2000; 2000GB-00003502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                     media and conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                      19; Conservative
                                                                                                          Denoel P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae
                                                                                                                              WPI; 2001-522599/57.
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 19 AA,
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WO200161013-A1
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                    23-AUG-2001
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The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein PS; (MoMP PS) of non-typeable H. influenzae (htth). Bach of these peptides contain an LB1(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP PS from strain ntHill28, representing amino acids Argl17 to Gly135. This peptide represents the third exposed loop of PS and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                  Recombinant bacterial outer membrane protein where one or more surface exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media and conjunctivitis:
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100.0%; Pred. No. 2.4e-09;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG80420 standard; protein; 353 AA
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                                                                                                                                                                                                                                                             Claim 2; Page 26; 29pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Conservative
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WPI; 2001-522599/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-657509/70.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABS66193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28 AA;
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The present invention relates to a new hyperblebbing Gram-negative bacterium genetically modified by one or more processes selected from down-regulating expression of one or more Tol genes and attenuating the peptidoglycan-binding activity by mutation of one or more gene (s) encoding a protein comprising a peptidoglycan-associated site. The invention is useful in a method of treatment of the human or animal body. The invention is also useful for protecting an individual against a bacterial infection. The invention has improved outer-membrane vesicles shedding properties. Blebs are more easily made in higher yield from the invention, and are more homogeneous in nature and can be more readily filter sterilised. The blebs can be made and harvested without the use of detergents such as deoxycholate, thus obviating chromatography control and ultra centrifugation steps. Vesicles prepared from the invention have reduced particle size (allowing sterile filtration through 0.22 mum pores), increased batch homogeneity, and a superior yield. The present manno acid asquence represents a Haemophilus influenzae protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes antigenic FS-like fimbrin subunit peptides (IB16f) peptides) of FS-like fimbrin proteins from various Haemophilus influenzes strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as octitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may alloc be used in vaccines against H. sifluenzae. Antibodies and probes from the present invention can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 98; DB 5; I 100.0%; Pred. No. 5.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY79979 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 30; 68pp; English
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                                                                                                                                                                                                                                                                                                                                              described in the invention
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 353 AA;
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for diagnosis of H. influenzae infection. AAY79955 to AAY79993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                         surface exposed loop; major outer membrane protein P5; MOMP P5;
outris media; sinusitis; conjunctivitis;
lower respiratory tract infection.
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                                                                                   Length 20;
                                                                                                            0; Indels
                                                                                  DB 3;
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                                                                                  Score 87.5; DB 3
Pred. No. 1e-07;
0; Mismatches
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/label= Loop 1
/note= "Extracellular domain"
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/label= Loop 3
/note= "Extracellular domain"
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/note= "Extracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                   AAB47447 standard; protein; 353 AA
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                                                                                                                                       1 RSDYKLYNKNSS-TLKDLGE 19
                                                                                                                                                        1 RSDYKLYNKNSSNTLKDLGE 20
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                                                                                  89.3%;
95.0%;
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                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .204
                                                                                  Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           media and conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-522599/57.
                                                         Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200161013-A1
                                                                                                                                                                                                                                                                                       31-OCT-2001
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                                                                                                                                                                                                                                                              AAB47447;
                                                                                                                                                                                                                                                                                                                 MOMP PS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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                                                                                                                                                               Non-typeable H. influenzae group 2 LB1(f) peptide NTHI-492.
                                                                                                                                                                                                                                  conjunctivitis; lower respiratory tract infection
                                                                                 AAY79975 standard; peptide; 21 AA
                                                                                                                                       15-MAY-2000 (first entry)
                                                                                                                                                                                                                                                           Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-116457/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                           28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1998;
                                                                                                                                                                                                                                                                                      WO9964067-A2
                                                                                                                                                                                                                                                                                                                 16-DEC-1999
                4
                                                                                                             AAY79975;
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Haemophilus influenza.
loop of PS and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Hamophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae, Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and
                                                                                                                                                                                                                                                                                                                                                                                Vaccine, non-typeable Haemophilus influenzae, ntHi; infection, chimeric protein, Haemophilus influenzae, P5-like fimbrin protein, lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis;
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                        Non-typeable H. influenzae group 2 LB1(f) peptide NTHI-506.
                                                                                                                        Score 87; DB 4; Length 353;
Pred. No. 4.3e-06;
; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          conjunctivitis; lower respiratory tract infection
                                                                                                               88.8%; Stor.
89.5%; Pred. No. ...
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                                                                                                                                                                                                                                                                         AAY79977 standard; peptide; 21 AA
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                                                                                                                                                                             1 RSDYKLYNKNSSTLKDLGE 19
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                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                 Query Match
Best Local Similarity 89.5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae
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                                                                                               Sequence 353 AA;
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Dequesne G,

Cohen J,

SMITHKLINE BEECHAM BIOLOGICALS. UNIV OHIO STATE RES FOUND.

99WO-US011980 98GB-00012613

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                                                                                                                                                                                                                  ofitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY19955 to AAY79931, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
                                                                                                                                                                                             aB
                                                                                                      The present invention describes antigenic PS-like fimbrin subunit peptides (LB1(f) peptides) of PS-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for disgnosis, prevention, and treatment of Haemophilus influenzae infections, such otitis media, sinusitis, conjunctivitis, or lower respiratory tract
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1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-typeable H. influenzae 1715MEE Group 2a type peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82;
                                                    Example 1; Page 30; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY79988 standard; peptide; 22 AA
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85.7%;
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Matches 18; Conservative
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                 the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 AA;
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Gaps

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0; Indels

1; Mismatches

1 RSDYKLYNKNS--STLKDLGE 19

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Score 82; DB 3; Length 21; Pred. No. 9.3e-07;

83.7%; 85.7%;

Query Match
Best Local Similarity 85.7
Matches 18; Conservative

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AAY79974;
           (SMIK)
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                                                                                                                                                                                                                              Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                             The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAX91201 to AAX91202, represent sequences used in the exemplification of the present invention
Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Hamphilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antiqenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ë,
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                                                                                                                                                                                                                                                                                                                                                                                                                            83.2%; Score 81.5; DB 3; Length 22;
81.8%; Pred. No. 1.2e-06;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                            Lobet
                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                           Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RSDYKLYNKNS---STLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSDYKLYNKNSSSNSTLKNLGE 22
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                                                                                                                                                                                                                                                                  Claim 3; Page 46; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY79983 standard; peptide; 22
                                                                                                                   99WO-US011980
                                                                                                                                       98GB-00012613
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nes 18; Conservative
                                                                                                                                                                                           Cohen J,
                                                   Haemophilus influenzae
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                                                                                                                                                                                                               WPI; 2000-116457/10.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 AA;
                                                                                                                                                                                           Bakaletz LO,
                                                                        WO9964067-A2
                                                                                                                  28-MAY-1999;
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Matches
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                                                                                                                                                                                                           Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
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                                                                                                                                                                                                                                                                                                                                                        The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY19955 to AAY19931, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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Pred. No. 1.2e-06;
1; Mismatches 0; Indels
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                                                                                       Lobet Y;
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SMITHKLINB BEECHAM BIOLOGICALS UNIV OHIO STATE RES FOUND.
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                                                                                       Dequesne G,
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81.8%;
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Best Local Similarity 81.8
Matches 18, Conservative
                                                                                          Bakaletz LO, Cohen J,
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peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as octifis anedia, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAZ91201 to AAZ91202, represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media and conjunctivitis.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LB1(f) containing peptide from strain ntHi-1715MEE (Group 2a type).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                                                                                                                                                                                                83.2%; Score 81.5; DB 3; Length 22; 81.8%; Pred. No. 1.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2001; 2001WO-EP001556.
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                                                                                                                                                                                                                                                                  Best Local Similarity 81.8
Matches 18; Conservative
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                                                                                                                                                                                                            Sequence 22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-OCT-2001
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AAB47440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant bacterial outer membrane protein where one or more surface-
exposed loops are modified is useful as a vaccine to prevent or treat
Haemophilus influenzae infection or associated disease, e.g., otitis
                                      Gaps
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                                                                                                                                                                                                                                                                                                                                    surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntH1; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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   Length 22;
                                                                                                                                                                                                                                                                                                    Entire 3rd loop from strain ntHi-1715MBE (Group 2a type).
                                      Indels
Score 81.5; DB 4;
Pred. No. 1.2e-06;
1; Mismatches 0;
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                                                                         1 RSDYKLYNKNS---STLKDLGE 19
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                                                                                                                                                                                             AAB47444 standard; peptide; 31 AA.
                                                                                             1 RSDYKLYNKNSSSNSTLKNLGE
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 83.2%;
81.8%;
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                                      18; Conservative
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                     Similarity
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   Query Match
Best Local
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RESULT 16

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conjunctivitis; lower respiratory tract infection.
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                                                                                                                                                                                                                                                                                                                                                                  Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.
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                                                                                                 Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Hamophilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-typeable H. influenzae group 2 LB1(f) peptide NTHI-495.
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                                                                            Plasmid LPD-LB1-III protein sequence.
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          AAY79993 standard; protein; 464 AA
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                                                      (first entry)
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                                                                                                                                                       Haemophilus influenzae
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Best Local Similarity
Matches 18; Conserva
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AAY79993
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes antigenic P5-like fimbrin subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.0%; Score 75.5; DB 3;
85.0%; Pred. No. 1.1e-05;
iive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                              Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 30; 68pp; English
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(OHIS ) UNIV OHIO STATE RES FOUND
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                                                                                                                                                                           99WO-US011980.
                                                                                                                                                                                                                                    98GB-00012613,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Cohen J,
Haemophilus influenzae.
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              Bakaletz LO,
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                                                         W09964067-A2
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                                                                Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                      The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. Influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes new DNA which encodes a chimeric protein containing: (i) the elicitor-binding site of an elicitor receptor; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         attack - comprises use of vector encoding chimeric protein containing elicitor-binding site of elicitor receptor together with signal transduction sequence of expression product of plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of transformant plants having increased resistance to fungal
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elicitor receptor, elicitor binding site; mould-resistant plant, chimeric protein; signal transduction motif; disease resistance;
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73
                                                                                                                                                                                                                                                                                                   76.5%; Score 75; DB 3; Length 21; 81.0%; Pred. No. 1.5e-05; ive 1; Mismatches 1; Indels
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            Lobet
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            Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW98912 standard; protein; 360 AA
                                                                                                      Example 1; Page 30; 68pp; English
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Best Local Similarity 81.v.
Best Local 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Umemoto N,
            Cohen J,
                                                                           Haemophilus influenza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-095341/08.
N-PSDB; AAX18559.
                                     WPI; 2000-116457/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal infection.
                                                                                                                                                                                                                                                                              Sequence 21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
            Bakaletz LO,
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which can confer disease resistance to plants. The elicitor receptor is a receptor for glucan, polygalacturonic acid. N-acetylketooligoascharide, elicitin, the expression product of the Avr gene of Clacosporium fulvum, or the expression product of the Avr gene of Clacosporium fulvum, or the expression product of the nipl gene of Rhynchosporium secalis. The signal transduction sequence may be a leucine-rich repeat, leucine zipper, nucleic acid binding site or serime/threonine kinase domain, preferably from the expression product of tomato Pto, Ptf, Cf-2 or Cf-9 gene, rice Xa21 gene, Arabidopsis thaliana RPS2 or RPM1 gene, or flax L6 gene, vectors from the present invention may be used for the production of plants, including crop plants and garden plants (such as rice, soybean, chrysanthemum, carnation or tobacco), with an increased resistance to moulds and other fungal infections. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes new DNA which encodes a chimeric protein containing: (1) the elicitor-binding site of an elicitor receptor; and (ii) the signal transduction sequence of the expression product of a gene which can confer disease resistance to plants. The elicitor receptor is a receptor for glucan, polygalacturonic acid, N-acetylketooligosaccharide, elicitin, the expression product of the Nvr gene of Clacosporium fulvum, or the expression product of the hipl gene of Rhynchosporium secalis. The signal transduction sequence may be a leucine-rich repeat, leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of transformant plants having increased resistance to fungal attack - comprises use of vector encoding chimeric protein containing elicitor-binding site of elicitor receptor together with signal transduction sequence of expression product of plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elicitor receptor; elicitor binding site; mould-resistant plant; chimeric protein; signal transduction motif; disease resistance;
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                                                                                                                                                                                                                                                                                  represents RPS2, given in the present invention
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7
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ed. No. 14;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 49;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                       50.0%;
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111 ADYKLCKKVSAILKSIGE
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Query Match
Best Local Similarity 55.0.,
Conservative
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                                                                                                                                                                                                                                                                                                                               Sequence 360 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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                                 preferably from the expression product of tomato Pto, Prf, Cf-2 or Cf-9 gene, rice Xa21 gene, Arabidopsis thaliana RPS2 or RPM1 gene, or flax L6 gene. Vectors from the present invention may be used for the production of plants, including crop plants and garden plants (such as rice, soybean, chrysanthemum, carnation or tobacco), with an increased resistance to moulds and other fungal infections. The present sequence represents ISER, given in the present invention
nucleic acid binding site or serine/threonine kinase domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Production of transformant plants having increased resistance to fungal attack - comprises use of vector encoding chimeric protein containing elicitor-binding site of elicitor receptor together with signal transduction sequence of expression product of plant disease resistance
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elicitor receptor, elicitor binding site, mould-resistant plant, chimeric protein; signal transduction motif; disease resistance;
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                                                                                                                                                                                                                            DB 2; Length 683; 32;
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                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                              Score 49;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW98914 standard; protein; 877 AA
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455 ADYKLCKKVSAILKSIGE 472
                                                                                                                                                                                                                                                                                                       2 SDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                              55.6%;
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Best Local Similarity 55.6
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KIRI ) KIRIN BEER KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungal infection.
                                                                                                                                                                                         Sequence 683 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                            RPS2; transgenic plant; Pseudomonas syringae plant pathogen;
disease resistance; crop improvement; Arabidopsis; tomato; soybean; bean;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pure DNA encoding an Arabidopsis thaliana Rps2 polypeptide - used to express the polypeptide in plant cells to provide disease resistance to
resistance to moulds and other fungal infections. The present sequence represents IER, given in the present invention
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Katagiri F;
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                                                                Length 877;
                                                                                         Indels
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/note= "AAAB not present in Seg ID:No.2"
350. .365
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505. .867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "leucine-rich repeat motif"
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                                                                5;
                                                                            ed. No. 44;
Mismatches
                                                                 Score 49;
                                                                             Pred. No.
                                                                                                                                                                                                                                                                                    Rps2 disease resistance polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                /note= "mature Rps2"
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 41-44; 88pp; English.
                                                                                                                                                                                                         AAR80132 standard; protein; 917 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu G;
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                                                                                                                                  :|||| | | : || :|| 649 ADYKLCKKVSAILKSIGE 666
                                                                                                                  2 SDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-00227360.
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                                                              50.0%;
                                                                             55.6%;
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Mindrinos MN, )
                                                                                                                                                                                                                                                          (first entry)
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                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
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N-PSDB; AAT04798.
                                                                                                                                                                                                                                                                                                                                      maize; wheat; rice.
                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                        Sequence 877 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 917 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-APR-1994;
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                                                                                                                                                                                                                                    AAR80132;
                                                                                                                                                                                                                                                                                                                                                                                         Key
Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
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The present invention describes new DNA which encodes a chimeric protein containing: (i) the elicitor-binding site of an elicitor receptor; and (ii) the signal transduction sequence of the expression product of a gene which can confer disease resistance to plants. The elicitor receptor is receptor for glucan, polygalacturonic acid, N-acetylketooligosaccharide, elicitin, the expression product of the Avr gene of Clacosporium fullvum, or the expression product of the nipl gene of Rhynchosporium secalis. The signal transduction sequence may be a leucine-rich repeat, leucine zipper, nucleic acid binding site or serine/threonine kinase domain,
                                                          AAR83440 is the complete amino acid sequence of the Rps2 (resistance to Pseudomonas syringae) protein derived from reading frame A as given in the specification. The Rps2 protein, antibody and oligonucleotide probes and primers can be derived from the Rps2 gene sequence (AAT01592). The oligonucleotides can be used for the identification and isolation of plant disease resistance genes such as the tomato Prf gene which may be used to transform a plant cell and produce a transgenic plant resistant to bacterial pathogens carrying the avrRpt2 avirulence gene. Antibodies may be used to screen recombinant expression libraries for Rps family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of transformant plants having increased resistance to fungal attack - comprises use of vector encoding chimeric protein containing elicitor-binding site of elicitor receptor together with signal transduction sequence of expression product of plant disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elicitor receptor; elicitor binding site; mould-resistant plant; chimeric protein; signal transduction motif; disease resistance;
                                                                                                                                                                                                                                                                                                                                              Length 965;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                            Score 49; DB;
Pred. No. 49;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 46-51; 109pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW98913 standard; protein; 1054 AA.
                      Disclosure; Fig 2; 241pp; English.
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119 ADYKLCKKVSAILKSIGE 136
                                                                                                                                                                                                                                                                                                                                                                                                                               2 SDYKLYNKNSSTLKDLGE 19
                                                                                                                                                                                                                                                                                                                                          50.0%;
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Best Local Similarity 55.6
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal infection.
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                                                                                                                                                                                                                                                                                                    Sequence 965 AA;
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/note= "all X residues correspond to stop codons present
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                                                                Gaps
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, Salmeron J;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Rps2; identification; isolation; primer; probe; plant disease; resistance gene; recombinant; avrRpt2; transgene.
                                                                                                                                                                                                                                                                                                                                                                                    A.thaliana RPS2 polypeptide from arbitrary reading frame A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= potential_membrane-spanning_domain
                    Score 49; DB 2; Length 917;
Pred. No. 46;
                                                              Indels
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1, Yu G, Baker B, Ellis J,
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|abel= kinase-la motif
note= "nucleotide binding site"
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/note= "nucleotide binding site"
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/label= kinase-2 motif
/note= "nucleotide bing site"
                                                            3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "DNA binding motif"
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US SEC OF AGRIC.
COMMONWEALTH SCI & IND RES ORG.
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|label= leucine-zipper
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/label= mat_protein
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/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                     AAR83440 standard; protein; 965 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in file AAT01592"
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119 ADYKLCKKVSAILKSIGE 136
                                                                                                      2 SDYKLYNKNSSTLKDLGE 19
                    55.6%;
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94US-00310912.
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Mindrinos MN,
               Query Match 50.0
Best Local Similarity 55.6
Matches 10; Conservative
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/label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-373764/48.
N-PSDB; AAT01592.
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22-SEP-1994;
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibite cellular proliferation; (8) identifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation; (8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
preferably from the expression product of tomato Pto, Prf, Cf-2 or Cf-9 gene, rice Xa21 gene, Arabidopsis thaliana RPS2 or RPM1 gene, or flax L6
               gene, rice Xa21 gene, Arabidopsis thaliana RPS2 or RPM1 gene, or flax L6 gene. Vectors from the present invention may be used for the production of plants, including crop plants and garden plants (such as rice, soybean, chrysanthemum, carnation or tobacco), with an increased resistance to moulds and other fungal infections. The present sequence represents CER, given in the present invention
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Xu HH:
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                                                                                                                                                                                 2; Length 1054;
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Forsyth F
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Yamamoto R,
                                                                                                                                                                                 Score 49; DB
Pred. No. 55;
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                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      ABU17574 standard; protein; 365 AA
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111 ADYKLCKKVSAILKSIGE 128
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Carr GJ,
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2001US-00948993.
2001US-0342923P.
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                                                                                                                                                                               55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                      10; Conservative
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus anthracis.
                                                                                                                                                                                                      Local Similarity
                                                                                                                                                 Sequence 1054 AA;
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Wall D,
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pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism actes; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the princed specification, but was obtained in the control of the princed specification, but was obtained to the control of the princed specification, but was obtained to the control of the princed specification, but was obtained to the control of the princed specification, but was obtained to the control of the princed specification, but was obtained to the control of the princed specification, but was obtained to the control of the princed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 365;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #3407.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 45804; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YKLYNKNSSTLKDL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 YKLYNKPFDKLKDL 27
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Best Local Similarity 71.4
Matches 10; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus anthracis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ACA21750.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200277183-A2.
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
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ID ABU1
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cc encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated pullphypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular to proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) capanism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling the extent or organism or (13) identifying the target of a compound that inhibits the compound that inhibits or confidentifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, confident in electronic formapart of the princed sequence is encoded by one of the trarget prokaryotic essential genes. Note: The sequence data for this patent did not form part of the princed sequences.

C ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.0%; Score 48; DB 6; Length 536;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 536 AA;
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interactions.

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                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                              Gaps
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              Disclosure; SEQ ID NO 9909; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                             Length 200;
                                                                                                                                                                                                                                                                                                               Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #9924.
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Yamamoto R,
                                                                                                                                                                                                                                                                       y Match 48.0%; Score 47; DB Local Similarity 47.4%; Pred. No. 15; hes 9; Conservative 3; Mismatches
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-07-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium botulinum.
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Trawick JD,
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                                                                                                                                                                                                                                            Sequence 200 AA;
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Wall
                                                                                                                                                                                                                                                                                                               Matches
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the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway consideration, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (1) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for identifying proceins or screening for homologous nucleic acids required for a callular proliferation to isolate candidate molecules for rational
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                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fixed problished_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPol Intron; DSM 10597; thermostable; DNA polymerase; 3'-5' exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 648;
98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA polymerase with 3'-5' exonuclease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 46; DB 6
; Pred. No. 98;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1118
/label= unknown
/note= "encoded by NTC"
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/note= "encoded by NTG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOEF ) BOEHRINGER MANNHEIM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKLYNKNSSTLKDLGE 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.98;
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Best Local Similarity 47.4.
Best Local Similarity 67.4.
Gonservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 648 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 29
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                                                 Thermostable DNA polymerase from Thermococcus sp. TY - useful for nucleic
                                                                                                                                  The present sequence (TYPO1 Intron) is a Thermococcus sp. TY (DSM 10597) thermostable DNA polymerase with 3'-5' exonuclease activity. The enzyme can specifically amplify nucleic acid fragments of up to 5 kb in high yields, has an activity half-life of 20 minutes at 90 degrees C, has an optimum temperature of 70-80 degrees C, has an optimum pH of 7.5, exhibits optimum activity at a KCl concentration of 80-100 mM, is magnesium ion-dependent and is inhibited by manganese ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant mutant Archeal DNA polymerase exhibiting an increased reverse transcriptase activity, useful for reverse transcribing an RNA template into cDNA or for amplifying an RNA template.
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                   Length 1829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermococcus strain TY DNA polymerase protein SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                   Pred. No. 3.6e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutant Archeal DNA polymerase; DNA polymerase; enzyme;
                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen CJ;
                                                                                                                                                                                                                                                                                                                      Score 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 13; 208pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADNS9952 standard; protein; 1829 AA.
                                                                                                     Claim 1; Page 5-8; 32pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorge JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-AUG-2003; 2003WO-US025762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-2002; 2002US-00223650.
12-MAY-2003; 2003US-00435766.
                                                                                                                                                                                                                                                                                                                   46.98;
                                                                                                                                                                                                                                                                                                                                   61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                             ||||:| : |||:
1161 KLYNENPNVLKDM 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         5 KLYNKNSSTLKDL 17
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reverse transcriptase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hogrefe H,
WPI; 1997-481494/45.
N-PSDB; AAT86433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004-376175/35.
                                                                    acid amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STRA-) STRATAGENE.
                                                                                                                                                                                                                                                                                  Sequence 1829 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADN59953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004039947-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN59952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arezi B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN59952
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type polynucleotide comprising an amino acid sequence selected from SEQ IONO:1-23 (odd numbers only); or (b) the chimeric polypeptide; (3) a composition comprising the mutant Archeal DNA polymerase exhibiting an increased reverse transcriptase activity, where the wild-type form comprises an amino acid sequence selected from SEQ ID NO:1-23 (odd numbers only); (4) a kit comprising a mutant Archeal DNA polymerase exhibiting an increased reverse transcriptase activity, where the wild-type form comprises an amino acid sequence selected from SEQ ID NO:1-23 (odd numbers only); and packaging materials; (5) reverse transcribing an RNA template, and (6) amplifying an RNA. The recombinant mutant Archeal DNA polymerase is useful for reverse transcribing an RNA template into cDNA polymerase is useful for maplifying an RNA template. The present sequence represents a DNA polymerase, which is used in the seguence represents a DNA polymerase, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine. cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activith/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cytokine, cell proliferation, cell differentiation, gene the
vaccine, pobtide therapy, stem cell growth factor, haematopoiesis,
tissue growth factor; immunomodulatory, cancer; leukaemia,
nervous system disorders, arthritis, inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 13980; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                      Score 46; DB 8; Length 1829;
Pred. No. 3.6e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA000088 standard; protein; 143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 13980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
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                                                                                                                                                                                                                                                                                                                                                        46.9%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1161 KLYNENPNYLKOM 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.0.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KLYNKNSSTLKDL 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                  Sequence 1829 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB, AAI80019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA000088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
      26666666666666666888
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenee), comprising one of 5481 sequencee (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a bill is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to recombinantly produce (I) and may be caid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distingialentifying
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                   part
   arthritis and
                                                                                                                                                                   Gaps
treatment of cancer, leukaemia, nervous system disorders, arthritis inflammation. Note: The sequence data for this patent did not form to the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C;
                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy
                                                       directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                             Length 143;
                                                                                                                                                                 Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V, Margarit Y RosI, Grandi G,
                                                                                                                                 4.
                                                                                                                             Score 45; DB 4
Pred. No. 22;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus polypeptide SEQ ID NO 9984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 4127; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                   ABP30404 standard; protein; 311 AA
                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001; 2001WO-GB004789
                                                                                                                             45.9%;
ilarity 53.8%;
Conservative
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                                                                                                                                                                                                     4 YKLYNKNSSTLKD 16
                                                                                                                                                                                                                          :|:|:|| |:||
52 HKVYSRNSQTVKD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) INST GENOMIC RES
                                                                                                              Query Match
Best Local Similarity
T; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPA
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                                                                                             Sequence 143 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR-) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    relford J.
                                                                                                                                                                                                                                                                                                                                                                       ABP30404;
                                                                                                                                                                                                                                                                                                   RESULT 32
                                                                                                                                                                                                                                                                                                                      ABP30404
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                                                                     ö
                                                                                                                                                                                                                                                                             Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Telford J, Masignani V, Margarit Y Rosl, Grandi G, Fraser C;
Tettelin H;
                                                                     ö
                                             DB 5; Length 311;
58;
                                                                     3; Indels
                                                                     5; Mismatches
                                                                                                                                                                                                                                                      Streptococcus polypeptide SEQ ID NO 3766.
                                              Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 3531; 4525pp; English.
                                                                                                                                                                               ABP27295 standard; protein; 315 AA
                                            45.98;
                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-2000; 2000GB-00026333.
                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-2001; 2001WO-GB004789.
                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                           :::||| || ::||
291 NWRLYNSNSGRMRDL 305
                                                                                             3 DYKLYNKNSSTLKDL 17
                                  Ouery Match
Best Local Similarity 46.77
Best Local 7; Conservative
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                             Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus proteins
Streptococcus proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABN67926.
                      Sequence 311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 315 AA;
                                                                                                                                                                                                                                                                                                                                                     WO200234771-A2.
                                                                                                                                                                                                                               02-JUL-2002
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                                                                                                                                                                                                      ABP27295;
                                                                                                                                                        RESULT 33
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertions.

The combination, of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian activity of a gene product, preferably enzymatic activity, carbon compound catabolism, blosynthetic, transporter, transcriptional, compound stabolism, blosynthetic, transporter, transcriptional, aginal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential candida albicans protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by
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                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
signal transduction; DNA replication; cell division; growth;
proliferation; Candida albicans; fungicide; antifungal.
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                                Length 315;
                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Candida albicans essential protein SEQ ID NO 7797.
                                5,
                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bussey H,
                                Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP73960 standard; protein; 624 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-DEC-2001; 2001WO-US049486.
                            45.9%;
ilarity 46.7%;
Conservative
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295 NWRLYNSNSGRMRDL 309
                                                                                                                                                                                           13
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                                                                                                                                                                                           DYKLYNKNSSTLKDL
WPI; 2002-566694/60.
N-PSDB; ABZ32510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200253728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2003
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RESULT 37
ADK34379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up care of whar-regulated in transgenic plants overexpressaing the heterodimeric step land factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, carey the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoraduplication, biochemistry, signal cransduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these each relative to the useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene represed 1.3 fold or more in plants overexpressing the EFFA/DPa transcription factor, given in an exemplification of the
                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                        Thale cress protein repressed in E2Fa/Dpa expressing plants SeqID 1794.
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                 plant, transgenic, E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                ;
                                                  Score 45; DB 5; Length 624;
Pred. No. 1.4e+02;
; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1794; 134pp; English
                                                                                                                                                                                                       ADN73899 standard; protein; 1017 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vlieghe K;
                                                                                                          1 RSDYKLYNKNSSTLKDLG 18
                                                                                                                           69 RDDYEFMIANPLTMKDLG 86
                                                     45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2002; 2002EP-00079408
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-2003; 2003WO-EP011658
the European Patent Office
                                                                                                                                                                                                                                                             (first entry)
                                                                Best Local Similarity 50.0
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Veylder L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CROP-) CROPDESIGN NV
                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1017 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADN73898
                            Sequence 624 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     WO2004035798-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nore proteins
                                                                                                                                                                                                                                                             15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nvention
                                                                                                                                                                                                                                  ADN73899
                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii lifection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Сарв
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent.
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45.5%; Pred. No. 2.1e+02;
tive 5; Mismatches 2; Indels 5
                        Length 1017;
                      Score 45; DB 8; 1
Pred. No. 2.5e+02;
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; SEQ ID NO 5599; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Acinetobacter baumannii protein #1473.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                       ADA34312 standard; protein; 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |:|| |:|| ||:|
RQDFKLMNQNTNTEDTIDLKEL
                                                                     4;
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                      45.9%;
                                                                                                                     3 DYKLYNKNSSTLKDLGE
                                                                                                                                                936 DTKLFLKSTFDIKDLGE
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter baumannii
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-576092/54.
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nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Breton G, Bush D;
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                                                                                                                                                                                                                                                                                                                                      ADA34312;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                           Arabidopsis thaliana protein fragment SEQ ID NO: 25961.
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9905-0137528P-
9905-0137524P-
9905-0138640P-
9905-0138847P-
9905-0139452P-
9905-0139453P-
9905-0139455P-
9905-0139455P-
9905-0139455P-
9905-0139455P-
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99US-0123180P.
99US-0125788P.
99US-012664P.
99US-0126785P.
99US-01207462P.
99US-01207449P.
99US-0130449P.
99US-0130449P.
99US-0130449P.
99US-0131449P.
99US-0131448P.
99US-0132487P.
99US-0132486P.
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99US-0139460P.
99US-0139461P.
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99US-0139463P.
99US-0139750P.
                                                                                                                                                                                                        25-FEB-2000; 2000EP-00301439
17-OCT-2000 (first entry)
                                                                                                                 Arabidopsis thaliana
                                                                                                                                              EP1033405-A2
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21-APR-1999;
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16-JUN-1999
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ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel isolated polynucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and thehat complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, nootropic, immunosuppressive, cytostatic, antipsoriatic, antinflammatory, antibacterial, antiviral, antibnessive autiparasitic activity. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases buck as archritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fungi or parasites. The present sequence is that of a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
                                                                                                                                                                                                                                               /note= "OTHER= All Xaa's in this sequence are unknown amino acids or the site of a stop codon within the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapa
                                                                    antiarthritic; antiparkinsonian; neuroprotective; nootropic; immunosuppressive; cytostatic; antipsoriatic; antiinflammatory; antibacterial; antiviral; antifungal, antiparasitic; gene therapy; arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus;
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Pred. No. 20;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 6461; 504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for treating, e.g., Parkinson's, Alzheim disease, and inflammatory bowel disease.
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG22869 standard; protein; 140 AA.
                                          Novel human polypeptide SegID6461.
                                                                                                                                                                                                                    1. .96
/label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2000; 2000US-00519705
19-MAY-2000; 2000US-00574454
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llarity 64.3%;
Conservative 1
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               (first entry)
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                                                                                                                                                                                                                                                                                 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKLYTKNYSRLHDL
                                                                                                                                              fungus; parasite; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-280918/32.
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hes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                      Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 96 AA;
                                                                                                                                                                                                                                                                                                          WO200216439-A2
                                                                                                                                                                             Homo sapiens
               06-MAY-2004
                                                                                                                                                                                                                                                                                                                                      28-FEB-2002
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Best Loc Matches

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RESULT 38

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Cyclopentanone 1,2-monooxygenase; CPMO; Pseudomonas; enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM50854 standard; protein; 550
99US-0151066P
99US-015103DP
99US-0151303P
99US-01513130P
99US-015303P
99US-015303P
99US-015303P
99US-015403P
99US-015403P
99US-015503P
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99US-015923P
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99US-015923P
99US-016908P
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99US-01609BP
99US-016193PP
99US-0161932P
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(first entry)
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27-AUG-1999

21-AUG-1999

10-SEP-1999

11-SEP-1999

11-SEP-1999

12-SEP-1999

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13-SEP-1999

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15-SEP-1999

16-SEP-1999

17-SEP-1999

18-SEP-1999

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01-MAY-2002
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Matches
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ID AAM5
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AAC AAM5
DT 29-P
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990S-0139763P.
990S-0139817P.
990S-0139817P.
990S-0140354P.
990S-0140354P.
990S-0140855P.
990S-0141281P.
990S-0141281P.
990S-0141281P.
990S-0141231P.
990S-0142308P.
990S-0144332P.
990S-0145331P.
990S-0145331P.
990S-0145331P.
990S-0146338P.
990S-014532P.
990S-0147302P.
990S-0144333P.
990S-0144332P.
990S-0144332P.
990S-0144332P.
990S-0144332P.
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990S-0144332P.
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990S-0144332P.
990S-0144332P.
18 - 70N - 1999;
22 - 70N - 1999;
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27 - 70N - 1999;
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30 - 70N - 1999;
30 - 70N - 1999;
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32 - AUG - 1999;
31 - AUG - 1999;
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Gaps

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Length 140;

Kruse UD, Kuester BD;

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The invention relates to multiprotein complexes from eukaryotes. Proteins of the invention and DNA sequences encoding them are given in records ABR52568-ABR53093 and ACC6010-ACC6194 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete document is available on CD-ROM
                                                                                                          New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
                                                                                                                                                                                                               Disclosure; SEQ ID NO 319; 17pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.9%; Score 44; DB 6;
60.0%; Pred. No. 4e+02;
tive 0; Mismatches
Bauer A, Gavin A, Grandi P, Krause R, K.
Marzioch M, Schultz JD, Superti-Furga GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: November 24, 2004, 09:21:45
Job time : 84.8152 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DYKLYNKUSSTLKDL 17
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                                                        WPI; 2003-250078/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1058 AA;
                                                                            N-PSDB; ACC60769
                                                                                                                                                                           disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of Comamonas (formerly Pseudomonas) sp. NCIMB 9872 cyclopentanone 1,2-monoxygenase (CPMO), as deduced from an isolated genomic DNA fragment (see ARA91715). CPMO carries out the second step of a degradation pathway that allows Comamonas sp. NCIMB 9872 to use cyclopentanol as a sole C-source for growth. CPMO protein (mol.wt. 62,111) shows 36.5% homology with the cyclohexanone 1,2-monoxygenase of Acinecobacter sp. NCIMB 9871. It was expressed in Escherichia coli as an IPTG-inducible protein. Isolated CPMO DNA, recombinant expression rectors, especially plasmids and viral DNA vectors, transformed cells, especially plasmids and viral DNA vectors, transformed cells, especially purified CPMO, recombinant CPMO and a method for growing cells in vitro in the presence of cyclopentanol or cyclopentanone as sole C-source, where the cells are transformed with an expression construct encoding enzymatically active CPMO, are all claimed. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                            Novel cyclopentanone monooxygenase from Comamonas having increased enzymatic activity for growing cells in a medium containing cyclopentanol or cyclopentanone as sole carbon source.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multiprotein complex; eukaryote; drug target; diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 27-28; 34pp; English
                                                                                                                                                                                           (CANA ) NAT RES COUNCIL CANADA.
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352 YEIFNONNVTLVDVNE 367
                                                                                                                                                     18-JUL-2000; 2000US-0218842P.
                                                                                                                13-JUL-2001; 2001WO-CA001032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein sequence #SEQ ID 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2001; 2001EP-00130253
Comamonas sp; 'NCIMB 9872'
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                                                                                                                                                                                                                                 Iwaki H, Hasegawa Y,
                                                                                                                                                                                                                                                                        WPI; 2002-179790/23.
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                                                                                                                                                                                                                                                                                        N-PSDB; ABA91715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 550 AA;
                                      WO200206452-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1258494-A1
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                                                                            24-JAN-2002.
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Matches
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Gaps

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Length 1058; 6; Indels Н

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November 24, 2004, 09:11:44 ; Search time 18:1739 Seconds (without alignments) 116.473 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                     Run on:
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112 1 RSDYKLYNKNSSSNSTLKNLGE 22 US-09-719-379A-2 **BLOSUM62** Perfect score: Scoring table: Sequence:

283416 segs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79: * 1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		trigger factor [im	hypothetical prote	probable membrane	hemorrhagic factor	hypothetical prote	hypothetical prote	calmodulin-like pr	probable integral	protein T7N9.14 [i	phage-related prot	hypothetical prote		hypothetical prote	opacity protein op				hypothetical prote	hypothetical prote	>	hypothetical prote	ы						probable membrane
SUMMARIES	QI t	C64187	C84985	T28904					T02109			C9703	T31345													87031	T1849	85969	857	S65004
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	Query Match Length	353	442	150	106	200	308	1374	324	332	700	2052	4767	103	182	234	238	241	246	285	338	430	481	583	611	1382	1619	1681	1758	1796
ď	Query Match	68.3	47.3	43.3	42.9	42.0	42.0	ä	41.1	•		41.1	41.1				•	40.2				40.2			٠	•	•	40.2	٠	40.2
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probable membrane	probable membrane	protein-tyrosine-p	tellurium resistan	uncharacterized co	hypothetical prote	hypothetical prote	hypothetical prote	peptide chain rele	clustered asparagi	zinc finger protei	hypothetical prote	probable regulator	beta-lactamase cla	hypothetical prote	hypothetical prote
863325	S64633	A54080	C75299	Н97060	T24854	T32211	T23572	A90525	A23535	T52382	G90569	846116	E97245	T18472	G86824
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40.2 1859			39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	39.3	38.8
	40.2			44 39.3	44 39.3		44 39.3			44 39.3		44 39.3	44 39.3	44 39.3	43.5 38.8

ALIGNMENTS

RESULT 1
C64187
outer membrane protein A homolog - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004
C; Accession: C64187
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID: 95350630; PMID: 7542800
A;Accession: C64187
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-353 <tigr></tigr>
A,Cross-references: UNIPROT:P43840; GB:U32796; GB:L42023; NID:g1574086; PIDN:AAC22819.1;
C;Superfamily: outer membrane protein A

Gaps 3, Query Match
68.3%; Score 76.5; DB 2; Length 353;
Best Local Similarity 77.3%; Pred. No. 0.0017;
Matches 17; Conservative 1; Mismatches 1; Indels

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132 RSDYKLYNENS---STLKKLGE 150 1 RSDYKLYNKNSSSNSTLKNLGE 22 q ઠ

C84985

trigger factor [imported] - Buchnera sp. (strain APS)

CiSpecies: Buchnera sp.
CiSpecies: Buchnera sp.
CiSpecies: Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 12-Jun-2003
CiAccession: C84985
Rishigenobu, S.; Watcanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A, Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A, Accession: C84985
A;Accession: C84985
A;Status: preliminary
A;Molecule type: DNA

A,Residues: 1-442 <STO>
A,Cross-references: GB:AP000398; GSPDB:GN00144
A,Experimental source: strain APS
C,Coss-references: A,Genetics: A,Gene: tig; BU474
C,Superfamily: FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor); BKBP-type

ö Gaps ö Query Match
47.3%; Score 53; DB 2; Length 442;
Best Local Similarity 56.2%; Pred. No. 5.4;
Matches 9; Conservative 4; Mismatches 3; Indels N

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A;Title: The complete amino acid sequence of the haemorrhagic factor LHFII, a metallopro A;Reference number: S15111; MUID:91224327; PMID:2026257
A;Accession: S15111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-308 «KLE»
A;Cross-references: UNIPROT:050827; GB:AE000788; NID:g2690123; PIDN:AAC66174.1; PID:g269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 'PRL',248,'K',250,'IDELTVIRLP',261,'SR',266-1374 <BOF>
A;Residues: 'PRL',248,'K',250,'IDELTVIRLP',261,'SR',266-1374 <BOF>
A;Residues: 'PRL',248,'K',250,'IDELTVIRLP',261,'SR',266-1374 <BOF>
A;Residues: PID:e190749; PID:g1326004
A;Residuental source: strain AB972
A;Residuental source: strain AB972
A;Note: the difference at the amino end is due to translation from the presumed intron s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YML133c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L0519; hypothetical protein L0532; hypothetical C;Species Saccharomyces cerevisiae
C;Date: 23-Aug-1996 #sequence revision 06-Sep-1996 #text change 09-Jul-2004
C;Accession: S69875; S58194; S58195; S50953; S50954; S64818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein BBK23 - Lyme disease spirochete plasmid K/lp36
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Scession: A70254
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Forn, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, R, Naturors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Fills: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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A;Accession: S69875
A;Accession: S69875
A;Residues: 1-1374 <BOW>
A;Residues: 1-1374 <BOW>
A;Cross-references: UNIPROT:Q03099; EMBL:Z50178; MIPS:YML133c
A;Experimental source: strain AB972
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                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-200 «FEB.»
A;Cross-references: UNIPROT: P22796
C;Superfamily: atrolysin C
C;Keywords: hydrolase; metalloproteinase; venom; zinc
F;140,144,150/Binding site: zinc (His) #status predicted
F;141/Active site: Glu #status predicted
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; Pred. No. 18;
3; Mismatches
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submitted to the EMBL Data Library, July 1995
A;Reference number: $58194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: | | |::| || || SNQDLINVQSAANDTLKTFGE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SDYKLYNKNSSSNSTLKNLGE 22
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Best Local Similarity 47.6%;
Matches 10; Conservative
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Best Local Similarity
                                                                                                                                         A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T25B6.3 - Caenorhabditis elegans
C;Species: T28904
R;Favello, A.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid T25B6.
A;Reference number: Z20541
A;Reference number: Z20541
A;Reference number: Z20541
A;Reference number: L78904
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;References: UNIPROT:Q22762; EMBL:U41546; PIDN:AAC48218.1; GSPDB:GN00028; CESP:TZ
A;Eross-references: UNIPROT:Q22762; EMBL:U41546; PIDN:AAC48218.1; GSPDB:GN00028; CESP:TZ
A;Genetics:
A;Gene
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probable membrane protein YPO0174 [imported] - Yersinia pestis (strain CO92)

C; Species : Versinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C; Accession: ABO022
R; Parkfill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: ABO001; MUID:21470413; PMID:11586360
A; Ascession: ABO022
A; Status: prellminary
A; Molecule type: DNA
A; Residues: 1-706 <KUR>
A; Residues: 1-706 <KUR>
A; Genetics:
A; Contact C; Genetics:
A; G
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$1511
hemorrhagic factor LHFII (EC 3.4.24.-) - bushmaster
c;Species: Lachesis muta muta (bushmaster)
c;Species: Lachesis muta muta (bushmaster)
c;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: $15111
R;Sanchez, B.F.; Diniz, C.R.; Richardson, M.
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46.2%; Pred. No. 8;
tive 3; Mismatches
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40.0%; Pred. No.
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DYERFNVNKASNTVLSSLNQ 562
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                                                                                                   388 KLYNKNKNLKNTMKNI 403
                                                        20
                                                    KLYNKNSSSNSTLKNL
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Matches 12, Conservative
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Best Local Similarity
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White Vugt, B.

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probable integral membrane protein PFB0790c - malaria parasite (Plasmodium falciparum) C; Species: Plasmodium falciparum C; Species: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004 C; Accession: B71606 R; Gardner, M.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 222, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:096251; GB:AE001418; GB:AE001362; NID:g3845275; PIDN:AAC7194
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaccession: E86397

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Hunter, J.L.; Y.; Liu, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: Aselfal; MUID:21016719; PMID:11130712

A;Accession: E86397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum A;Reference number: A71600; MUID:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                   Length 324;
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42;
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Pred. No. 90;
2; Mismatches
                                                                                                                                                                                                       5; Mismatches
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Pred. No.
                                                                                                                                                               Pred. No
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                                                                                                                                                                                                                                                                                           1 RSDYKLYNKNSSSNSTLKNLG 21
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38.1%;
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57.1%;
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Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                       Conservative
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A,Map position: 2
A,Introns: 26/1; 115/1; 205/1
                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-700 <S
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                                                A;Residues: 1-265,"HVCCPS' <BOA>
A;Cross-references: EMBL:Z50178; NID:g927528; PIDN:CAA90550.1; PID:g927529
A;Experimental source: strain AB972
A;Note: the difference at the carboxyl end is due to translation from the presumed intro R;Wedler, H.; Wambutt, R.
B;Wedler, H.; Wambutt, R.
Bubmitted to the EMBL Data Library, January 1995
A;Description: Sequence of a 37 kb DNA fragment from chromosome XII of Saccharomyces cer A;Reference number: S50950
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-324 <ROUJ.
A;Cross-references: UNIPROT: P25071; EMBL: AC004261; NID: g3402695; PID: g3402707
A;Experimental source: cultivar Columbia
A; Molecule: A;Experimental source: cultivar C: M; Venter, J
A;Reference number: A84420; MuID: 20083487; PMID: 10617197
A;Residues: 1-324 <STO>
A;
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A,Residues: 170-278,'G',280-329,'D',331-432,'G',434-824,'N',826-1072,'G',1074-1374 <WEW>
A,Cross-references: EMBL:273171; NID:g1360281; PIDN:CAA97520.1; PID:e245485; PID:g136028
A,Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: Closely related hypothetical proteins containing similar 12-residue repeats are C;Keywords: tandem repeat; transmembrane protein P;414-430/Domain: transmembrane #status predicted <TVM> P;414-430/Domain: transmembrane #status predicted <TVM> F;847-966/Region: 12-residue repeats (T-T-T-[EKA]-[SG]-[TI]-[ND]-[ASV]-[TRSNK]-T-[NS]-[A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Rosidues: 170-278, G',280-329,'D',331-432,'G',434-824,'N',826-1072,'G',1074-1374 <WED>
A;Cross-references: EMBL:247973; NID:9642313; PIDN:CAA87990.1; PID:9642317
A;Accession: S50954
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N;Alternate names: calmodulin-related protein T3K9.13
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C;Accession: T02109; G84837
K;Rounaley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, February 1999
A;Description: Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence.
A;Reference number: Z14570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-265,/HV', 766-767,'P', 769 <WEF>
A; Residues: 1-265,/HV', 766-767,'P', 769 <WEF>
A; Crogsdues: 1-265,/HV', 766-767,'P', MD: 9642313; PIDN: CAA87989.1; PID: e135624; PID: g642316
R; Wedder, H; Wedler, E.; Scharfe, MD: Wambutt, R.
Bubmitted to the Protein Sequence Database, May 1996
A; Reference number: S64792
A; Accession: S64818
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Best Local Similarity 71.4%;
Matches 10; Conservative
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A,Gene: TCH3; T3K9.13; At2g41100
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A;Title: Peculiar feature of the organization of rRNA genes of the Chlorella chloroplast A;Reference number: A93622; MUID:86232622; PMID:3714498
A;Accession: D24444
                                                                                                                                                                                                                                            A)Genome: chloroplast
C;Superfamily: Chlorella ellipsoidea chloroplast hypothetical protein 4 (16S-23S rRNA sp
C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-234 <KUP>
A;Cross-references: UNIPROT:Q04885; EMBL:Z18940; NID:g49336; PIDN:CAA79373.1; PID:g94080
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A;Note: expression of opacity proteins is regulated by the number of translated repeat e
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:018058; EMBL:Z82282; PIDN:CAB05271.1; GSPDB:GN00022; CESP:T0
A;Experimental source: clone T07G12
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NiAlternate names: outer membrane protein opa65
C;Species: Neisseria gonorrhoeae
A;Variety: strain VP1
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 336438; Z28617
R;Kupch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell of the cession: 336348; MUID:93178439; PMID:8440254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypochetical protein T07G12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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C;Superfamily: calmodulin; calmodulin repeat homology
C;Reywords: EF hand
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A;Molecule type: DNA
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Pred. No. 31;
7; Mismatches
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R;Cummings, P.
Bubmitted to the EMBL Data Library, November 1996
A;Reference number: Z19921
A;Accession: T24672
                                                                                                                                                                                                                                                                                                                                                                                     ; Score 45.5; DE; Pred. No. 15; 3; Mismatches
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                                                                                                             A;Molecule type: DNA
A;Residues: 1-103 <YAM>
A;Cross-references: UNIPROT:P05721
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                     40.6%;
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Best Local Similarity 48.0°
Matches 12; Conservative
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les 7; Conserv
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Matches
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                                                                                                                              C97038
phage-related protein, Yqbo B. subtilis homolog [imported] - Clostridium acetobutylicum
C59038
c59edias: Clostridium acetobutylicum
C5 Specias: Clostridium acetobutylicum
C5 Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C5Accession: C97038
R50011ng, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
C5 Bacteriol. 183, 4823-4838, 2001
Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97038
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Roccession: C97038
A;Residues: 1-2052 -KURP
A;Residues: 1-2052 -KURP
A;Residues: 1-2052 -KURP
A;Residues: 1-2052 -KURP
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1120
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R;Yamada, T.; Shimaji, M.
Nucleic Acids Res. 14, 3827-3839, 1986
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Pred. No. 6.5e+02;
4; Mismatches 6; Indels
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Pred. No. 2.7e+02;
4; Mismatches 2;
          139 SDFKFIFSTVSSNETLEKLG 158
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55.6%;
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Best Local Similarity 47.4%;
Matches 9; Conservative 4
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Best Local Similarity
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-241 «JOH» A;Esidues: 1-241 «JOH» A;Cross-references: UNIPROT: 039778; EMBL: U30506; NID: 91000085; PIDN: AAB03080.1; PID: 91000 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant Mol. Biol. 30, 297-306, 1996
A,Title: Structural characterization of genes corresponding to cotton fiber mRNA, E6: re.
K,Reference number: S65061; MUID:96178868; PMID:8616253
A,Accession: S65063
A,Status: nucleic acid sequence not shown; translation not shown
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CTORS-references: UNIPROT:Q42488; EMBL:U30507; NID:g1000087; PIDN:AAB03081.1; PID:g100:
CTORS-references: UNIPROT:Q42488; EMBL:U30507; NID:g100087; PIDN:AAB03081.1; PID:g100:
Experimental source: cultivar Sea Island; clone SIE6-2A
Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
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C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C; Accession: C97178
C; Accession: C97178
R; Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J: Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
Bacteriol. 183, 4823-4938, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A; Reference number: A96900; MUID:21359325; PMID:21359325
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A;Experimental source: Clostridium acetobutylicum ATCC824
        E6:
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A;Experimental source: cultivar Sea Island; clone SIE6-3B
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
    A,Title: Structural characterization of genes corresponding to cotton fiber mRNA, A,Reference number: S65061; MUID:96178868; PMID:8616253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
40.2%; Score 45; DB
Best Local Similarity 45.0%; Pred. No. 42;
Matches 9; Conservative 4; Mismatches
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DYKLYNKNSSSNSTLKNLGE 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary A;Molecule type: DNA
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                                                                                                  A; Accession: S65062
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46130; S65061
R;John, M.E.; Crow, L.J.
R;John, M.E.; Crow, L.J.
A;Title: Gene expression in cotton (Gossypium hirantum L.) fiber: cloning of the mRNAs.
A;Reference number: A46130; MUID:92335179; PMID:1631059
A;Accession: A46130
A;Accession: A46130
A;Accession: A46130
A;Accession: A66130
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A;Experimental source: cv. Coker 312
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A;Experimental source: cv. Coker 312
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
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A;Molecule type: DNA
A;Residues: 1-238 <JO2>
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Plant Mol. Biol. 30, 297-306, 1996
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A;Note: sequence extracted from NCBI backbone (NCBIN:108417, NCBIP:108418)
R;John, M.E.
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llarity 45.0%; Pred. No. 41;
Conservative 4; Mismatches 7; Indels
                                                          opa65 #status predicted <MAT>
C;Keywords: cell surface component; transmembrane protein F;1-234/Froduct: opacity protein opac5 #status predicted <MA; F;11-19/Domain: transmembrane #status predicted <TM1>F;20-51/Domain: extracellular #status predicted <TM1>F;20-51/Domain: extracellular #status predicted <EXT1>F;20-51/Domain: transmembrane #status predicted <TM2>F;52-60/Domain: transmembrane #status predicted <TM2>F;52-11/Domain: transmembrane #status predicted <TM3>F;72-107/Domain: extracellular #status predicted <TM3>F;72-107/Domain: transmembrane #status predicted <TM4>F;108-122/Domain: transmembrane #status predicted <TM5>F;108-125/Domain: transmembrane #status predicted <TM5>F;14-176/Region: hypervariable region HV2
F;186-198/Domain: transmembrane #status predicted <TM6>F;14-176/Region: hypervariable region HV2
F;186-198/Domain: extracellular #status predicted <TM6>F;102-210/Domain: extracellular #status predicted <TM7>F;126-225/Domain: extracellular #status predicted <TM7>F;226-234/Domain: extracellular #status predicted <TM8>
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hes 9; Conserve
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us-09-719-379a-2.rpr

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probable secretion/efflux ABC transporter, ATP-binding protein - Helicobacter pylori (st C; Species: Helicobacter pylori
A; Variety: strain 999
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C; Accession: A71918
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Javes, C.; Gibbon, R.; Marberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; A; Tite: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
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A;Experimental source: strain J99
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C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
F;363-562/Domain: ATP-binding cassette homology <ABC>
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A;Molecule type: DNA
A;Residues: 1-481 «LAW»
A;Cross-references: UNIPROT:077353; EMBL:AL008970; NID:e1407852; PIDN:CAA15608.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C0475c - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-06t-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004 C;Accession: T18465 C;Accession: T0865 Barrell, B. S;Lawson, D.; Bowman, S.; Barrell, B. submitted to the EMBL Data Library, November 1998
                                                                                                                                                         Gaps
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hypothetical protein Y4851B.4 - Caenorhabditis elegans
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40.2%; Score 45; DB 2; 1
Best Local Similarity 58.8%; Pred. No. 1.1e+02;
Matches 10; Conservative 1; Mismatches 6;
                                                                            DB 2;
76;
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Pred. No.
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Pred. No.
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Best Local Similarity 41.2%;
Matches 7; Conservative
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A; Accession: T18465
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                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                     3 DYKLYNKNS
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    A;Note: MSV157
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                                                                                                                                                                                                                                                                                                                                                                   National protein YBR050c - yeast (Saccharomyces cerevisiae)
Nathernate names: Mypothetical protein YBR0504
C. Species: Saccharomyces cerevisiae
C. Saccession: S45908; S45505; S55849
R. Alinovic, G. Pebl, F.M.; Pebl, T.M.
Submitted to the Protein Sequence Database, August 1994
A. Reference number: S45908
A. Accession: S45908
A. Accession: Saccharomyces cerevisia
A. Accession: Saccenter and analysis of 24 kb on chromosome II of Saccharomyces cerevisiae
A. Accession: S49503
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALL2
A. Accession: S49503
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALL2
A. Accession: S49503
A. Molecule Lype: DNA
A. Accession: S49503
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALLA
A. Accession: S5849
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALLA
A. Accession: S5846
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALLA
A. Accession: S5846
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALLA
A. Accession: S5846
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALLA
A. Accession: S5849
A. Molecule Lype: DNA
A. Residues: 1-1318 - ALLA
A. Accession: S5849
A. Molecule Lype: DNA
A. Molecule Lype: DNA
A. Residues: DNA
A. Residues: 1-1318 - ALLA
A. Accession: S5849
A. Molecule Lype: DNA
A. Molecule 
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ORF MSV157 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
ORF MSV157 hypothetical protein - Melanoplus sanguinipes entomopoxvirus
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28318
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
A;Virol. 73, 533-552, 1999
A;Yitle: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28318
A;Accessio
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40.2%; Score 45; DB 2; Length 338;
Best Local Similarity 58.8%; Pred. No. 59;
Matches 10; Conservative 3; Mismatches 0; Indels
                                            1; Indels
        Pred. No. 50;
0; Mismatches
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90.06;
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                    5 KLYNKNSSSN 14
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4,Molecule type: DNA
4,Residues: 1-1681 <WED>
4,Cross-references: UNIPROT:P40105; EMBL:U34775; NID:g971260; PIDN:AAB65037.1; PID:g9712
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NyAlternate names: hypothetical protein J0202; hypothetical protein L9122.1-a; hypothetical protein Y19402.01c; protein HRD1054; protein HRD732
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence revision 08-Sep-1995 #text change 09-Jul-2004
C;Accession: S57015; S51848; $50702; S45147; S50349; S31214; S59002; S48919; S69476; S58
Rivandenbol, M.; Durand, P.; Portetalle, D.; Hilger, F.
Submitted to the Protein Sequence Database, September 1995
A;Reference number: S56835
A;Accession: S57015
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A; Residues: 1-1758 <VAN>
A; Cross-references: UNIPROT: P40889; EMBL: Z49500; NID: 91015618; PID: 91017444; MIPS: YJL225
A; Caross-references: Unirand, P.; Portetelle, D.; Hilger, F.
Submitted to the EMBL Data Library, January 1995
A; Description: Sequence analysis of yeast chromosome X left telomere.
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Note: Closely related hypothetical proteins containing similar 12-residue repeats are
C;Keywords: tandem repeat
P;1155-1274/Region: 12-residue repeats (T-T-T-[EKA]-[SG]-[TI]-[ND]-[ASV]-[TRSNK]-T-[NS]-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S59693; S50693
R;Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, August 1995
A;Description: Sequence analysis of chrV right subtelomeric region.
A;Reference number: S59693
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A;Description: The sequence of S. cerevisiae cosmids 9163 and 9132.
A;Reference number: SS0431
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    yeast (Saccharomyces cerevisiae)

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40.2%; Score 45; DB 2; Length 168
Best Local Similarity 58.8%; Pred. No. 3.1e+02;
Matches 10; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                       Score 45; DB 2;
Pred. No. 3e+02;
4; Mismatches
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                                                                                                                                                                                                                                             40.2%;
53.8%;
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Best Local Similarity
Matches 7; Conserv
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A;Residues: 1-738 <DIE>
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                                A;Map position: 3
A;Introns: 87/3
A;Note: C0770c
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27013
R;Accession: T27013
R;Accession: T27013
A;Reference number: Z20299
A;Reference number: Z20299
A;Accession: T27013
A;
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A;Map position: 12R
A;Note: (10sely related hypothetical proteins containing similar 12-residue repeats are
C;Keywords: tandem repeat
F;855-974/Region: 12-residue repeats (T-T-T-[EKA]-[SG]-[TI]-[ND]-[ASV]-[TRSNK]-T-[NS]-[A
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C;Species: Saccharomyces cerevisiae
C;Species: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S70310
R;Wedler, H.; Wambutt, R.
submitted to the Protein Sequence Database, August 1995
A;Reference number: S70306
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A,Map position: 2
A,Introns: 59/2; 80/3; 144/3; 413/3
C,Superfamily: Caenorhabditis elegans hypothetical protein Y48E1B.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 40.2%; Score 45; DB 2; Length 611; Best Local Similarity 40.0%; Pred. No. 1.1e+02; Matches 8; Conservative 5; Mismatches 7; Indels
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A;Residues: 1-1382 <WED>
A;Cross-references: UNIPROT:O13559; MIPS:YLR466w
A;Note: experimental_source strain $288C
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||:|||:| : :| | 97 NDYELYNRNLLATRFFENSG 116
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submitted to the Protein Sequence Database, May 1996
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                                           A, Reference number: $64792
A, Accession: $65339
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Matches 10; Conserv
                                                                                                                                                                                                                                                                                                     A; Accession: S56191
A; Molecule type: DNA
A; Residues: 1-65,'N',
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A Notest these "Wildyward Prepaying Practicage (1912); projections of intron agenetic and another internation and active active and active active and active active
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N; Alternate names: hypothetical protein D3703.4; hypothetical protein L9040; hypothetical C; Species: Saccharomyces cerevisiae C; Species: Saccharomyces cerevisiae C; Date: 01-Aug-1995 #sequence rerevision 24-May-1996 #text_change 09-Jul-2004 C; Accession: S65004; S67814; S62024 R; Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R. submitted to the Protein Sequence Database, May 1996 A; Reference number: S64792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-65,'N',67-73,'I',75-84,'Q',86-150,'PCPG',439,'LS',442,'NSECQ',448,'ERQL',4
A;Gross-references: EMBL:D44603; NID:g871957; PIDN:BAA08055.1; PID:d1008646; PID:g871962
R;Dietrich, F.S.
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                                                                                                                                                                                                 Sasanu
                                                                                                                                                                                                                                                                                          chromosome VI from Saccaromyces ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residues: 1-65,'N',67-73,'I',75-84,'Q',86-150,'PCPG',439,'LS',442,'NSECQ',448,'ERQL',4;
Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09177.1; PID:d1009815; PID:g836691
A; Molecule type: DNA
A; Residues: 'ICTCTAQLIHILNSLIITFSDDDKTETGQSFVYIDGFLVKKGHNNQHTIVNFETYKOKY',1-73,'I',75-84,'
A; Residues: 'ICTCTAQLIHILNSLIITFSDDDKTETGQSFVYIDGFLVKKGHNNQHTIVNFETYKOKY',1-73,'I',75-84,'
A; Cross-references: BMBL: 273537; MIPS: YPR302w
A; Experimental source: strain $288C (AB972)
B; Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu Bubmitted to the EMBL Data Library, May 1995
A; Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces ce
A; Reference number: $56186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmids 9669, 9163, 9132, 8334, 8199, and A; Reference number: 850514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-73,'I',75-84,'Q',86-104,'NK',912,'RDGLH',918-919,'S',921,'AYF',925,'IQ' <
A;Residues: 1-73,'I',75-84,'Q',86-104,'NK',912,'RDGLH',918-919,'S',921,'AYF',925,'IQ' <
A;Cross-references: EMBL:U18922; NID:g603405; PID:g603430; GSPDB:GN00005; MIPS:YER189w
R;Kirsten, J.
R;Kirsten, J.
Submitted to the EMBL Data Library, March 1995
A;Description: The sequence of S. cerevisiae cosmid 9122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: DNA
;Residues: 1-104, NK', 912,'RDGLH',918-919,'S',921,'AYF',925,'IQ' <DIE>
;Cross-references: EMBL:U18795; NID:g603241; PID:g603243; GSPDB:GN00005; MIPS:YEL075c
;Accession: $50692.
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A;Residues: 1-64 «KIR»
A;Cross-references: EMBL:U22383; GSPDB:GN00012; MIPS:YLR462w
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A;Map position: 5L; 5R; 6L; 8L; 9L; 10L; 12R; 15R; 16R
A;Introns: 387/3
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58.8%; Pred. No. 3.3e+02;
tive 0; Mismatches 7;
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C;Keywords: tandem repeat; transmembrane protein
F9.8-24/Domain: transmembrane #status predicted <TM1>
F9.90-916/Domain: transmembrane #status predicted <TM2>
F19333-1452/Region: 12-residue repeats (T-T-T-[EKA]-[SG]-[TI]-[ND]-[ASV]-[TRSNK]-T-[NS]-
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F;900-916/Domain: transmembrane #status predicted <TM2>
F;1333-1452/Region: 12-residue repeats (T-T-T-[EKA]-[GG]-[T1]-[ND]-[ASV]-[TRSNK]-T-[NS]-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein YGR296w - yeast (Saccharomyces cerevisiae)

NyAlternate names: hypothetical protein G9608; hypothetical protein P0254; hypothetical

Species: Saccharomyces cerevisiae

Dibate: 17-May-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004

Matson, M.D.

Submitted to the Protein Sequence Database, May 1996
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Residues: 17.859 < WEW>
Residues: 17.859 < WEW>
Residues: 17.859 < WEW>
Residues: 17.859 < WEW
Residues: 18.851; MIPS:YPL283C; NID:gl37058l; PID:e246989; PID:gl370582
Residuental source: strain S288C (AB972)
Residuentics: CH16
Residuentics: CH16
Residuentics: Residuence Database, May 1996
Reference number: 864967
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                                                                                                                                                      Length 1859;
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"Molecule type: DNA

"Residues: 1-1052 <WAT>

"Residues: 1-1052 <WAT>

"Cossereferences: UNIPROT:P53345; EMBL:Z73081; MIPS:YGR296w

"Experimental source: strain $288C

"Genetics: CH7

"Medler, H.; Scharfe, M.; Wedler, E.; Wambutt, R.

ubmitted to the Protein Sequence Database, May 1996

"Reference number: $64356
                                                                                                                                                   / Match 40.2%; Score 45; DB 2; Length 185
Local Similarity 58.8%; Pred. No. 3.5e+02;
Nes 10; Conservative 0; Mismatches 7; Indels
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58.8%; Pred. No. 3.5e+02;
ive 0; Mismatches 7; Indels
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Medler, H.; Wedler, B.; Scharfe, M.; Wambutt, R.
Demitted to the Protein Sequence Database, May 1996
Reference number: S64792
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;Residues: 1-813 -CBL>
;Cross-references: EMBL:273521; MIPS:YPL283C
;Experimental source: strain S288C (A8972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 586-1859 <WED>
Cross-references: EMBL:Z73081; MIPS:YGR296w
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Best Local.Similarity
Matches 10; Conserv
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A,Map position: 16L
A,Introns: 7/1
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                                                                                                                                                          Query Match
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A; Molecule type: DNA
A; Residues: 1-1796 < MED>
A; Residues: 1-1796 < MED>
A; Residues: 1-1796 < MED>
A; Cross-references: UNIPROT: P24088; EMBL: Z73327; MIPS: YLR467w; NID: g1360589; PID: e245588, A; Experimental source: strain S288C
A; Genetics: CH12
A; Genetics: CH12
A; Genetics: CH2
A; Genetics: CH2
A; Genetics: CH2
A; Reference number: Sequence Database, July 1996
A; Reference number: S67608
A; A; Cossion: S67814
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R;Dietrich, F.S.; Mulligan, J.; Allen, E.; Araujo, R.; Aviles, E.; Berno, A.; Carpenter,
H.; Lin, D.; Mosedale, D.; Nakahara, K.; Namath, A.; Oefner, P.; Oh, C.; Petel, F.X.; Ro
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A;Note: Closely related hypothetical proteins containing similar 12-residue repeats are
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F;836-852/Domain: transmembrane #status predicted <TMM>
F;1269-1388/Region: 12-residue repeats (T-T-[EKA]-[SG]-[TI]-[ND]-[ASV]-[TRSNK]-T-[NS]
                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Realdudes: 1-1796 «WAN»
A;Crose-references: EMBL:274389; MIPS:YDR545w; NID:g1431573; PID:e253351; PID:g1431574
A;Experimental source: strain S288C
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probable membrane: hypotherical protein N0152
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces fiscapenere_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S63325; S63326
R;Obermaier, B.; Piravandi, E.; Rinke, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63317
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A,Readidues: 1-916 <0DB-
A,Cross-references: UNIPROT:P53819; EMBL:Z71615; MIPS:YNL339c
A,Experimental source: strain S288C
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X;Residues: 1-228 cDIBs.
A;Crose.references: EMBL:U43834; NID:gl165292; PID:gl165300
A;Experimental source: strain AB972
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submitted to the Protein Sequence Database, April 1996
A;Reference number: S63326
A;Accession: S63326
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58.8%; Pred. No. 3.3e+02;
tive 0; Mismatches 7;
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A;Reference number: S62017
A;Accession: S62024
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A;Reaidues: 8-1859 wBED>
Zross-references: EMBL:Z71615; MIPS:YNL339c
A;Experimental source: strain S288C
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A;Map position: 14L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 58.8
les 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 12R
A;Note: YLR467w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: SGD:YRF1-6
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C,Genetics: <CH12>
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 131, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325, PMID:21359325
                                                                                                                                                                                             A;Residues: 1-252 <KUR>
A;Cross-references: UNIPROT:097JH9; GB:AE001437; PIDN:AAK79275.1; PID:g15024234; GSPDB:GR
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:Q22421; EMBL:Z73911; PIDN:CAA98140.1; GSPDB:GN00022; CESP:T12
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A;Cross-references: EMBL:AF022980; PIDN:AAB69913.1; GSPDB:GN00023; CESP:T03D3.7
A;Experimental source: strain Bristol N2; clone T03D3
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricenard, N.
Submitted to the EMBL Data Library, June 1996
Submitted to unber: 219943
A;Reference number: 219943
A;Accession: T94854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DMA
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ilarity 40.9%; Pred. No. (
Conservative 4; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44;
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A;Introns: 63/3; 186/3; 202/1; 258/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 86/2; 192/3; 231/2
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Matches 9; Conserv
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                                                                                                                                                        A; Accession: H97060
A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                          protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - chicken C; Species: Gallus gallus (chicken)
C; Species: O2-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C; Accession: A54080; I50592
R; Fang, K.S.; Barker, K.; Sudol, M.; Hanafusa, H.
J. Biol. Chem. 269, 14056-14063, 1994
A; Title: A transmembrane protein-tyrosine phosphatase contains spectrin-like repeats in A; Reference number: A54080; MUID:94245724; PMID:818866
A; Accession: A54080
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1237 cFAN>
A; Cross references: UNIPROT:Q91976; EMBL:Z21960; NID:G510510; PIDN:CAA79972.1; PID:G5105
C; Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase F; S28-1170/Domain: leukcyte common antigen cytosolic domain homology cLAC>
F; G10-834/Domain: protein-tyrosine-phosphatase homology cPTP>
F; G10-834/Domain: cys (phosphocyteine intermediate) #status predicted
F; 792/Binding site: cys (phosphote (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 33
C75299
tellurur resistance protein TerD - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: C75299
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S; Smith, H.O.; Vener, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75299
A;Status: prediminary
A;Recession: C75299
A;Status: DNA
A;Residues: 1-191 < AMA
A;Residues: 1-191 < AMA
A;Residues: UNIPROT:Q9RSA5; GB:AE002055; GB:AE000513; NID:g6460024; PIDN:AAF1176
A;Cross-references: UNIPROT: Q9RSA5; GB:AE002055; GB:AE000513; NID:g6460024; PIDN:AAF1176
A;Cross-references: UNIPROT: A;Map position: 1
C;Superfamily: tellurium resistance protein terD
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uncharacterized conserved protein, probable metal-binding CAC1304 [imported] - Clostridi
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97060
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DYGNIEEKNNSAEVTLKNLKE 171
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         | ||| || || 603 YTDYNKNGSSEPRLKTL 619
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hes 7; Conserv
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 7; Conserva
                                                                                                                     A; Molecule type: DNA
A; Residues: 1-451 < WAH>
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A;Status: preliminary
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A;Cross-references: UNIPROT:Q21417; EMBL:275545; PIDN:CAA99885.1; GSPDB:GN00019; CESP:K1
A;Experimental source: clone K10D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide chain release factor 1 (rf-1) [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: A90525
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A;Experimental source: strain UAB CTIP
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clustered asparagine-rich merozoite-associated antigen - malaria parasite (Plasmodium fa
C;Species: Plasmodium falciparum
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A90525
C;Accession: A90525
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
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                                                                                                                                                                                                                                    Cispecies: Caenorhabditis elegans
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T23572
Rimchurasy, A.
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    Length 312;
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88;
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                                            Indels
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                                                                                                                                                                                                                  - Caenorhabditis elegans
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A;Molecule type: DNA
    Score 44; DB 2;
Pred. No. 76;
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                                        3; Mismatches
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                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, June 1996
A;Reference number: 219762
A;Accession: T23572
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Pred. No. 8
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Pred. No.
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C,Superfamily: translation releasing factor
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A;Introns: 46/2; 83/2; 169/3; 241/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 YEVYRKSSFKKSTIKRL 252
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    39.3%;
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Local Similarity 47.1%;
Les 8; Conservative
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Best Local Similarity 42.5-
Best Local 9, Conservative
                                                                                                  299 KIYNKNSTSSIT 310
                                            Conservative
                                                                                5 KLYNKNSSSNST 16
                                                                                                                                                                                                                    hypothetical protein K10D3.3
Query Match
Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-359 < KUR>
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Best Local S
Matches 8
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A;Cross-references: UNIPROT:P13824; GB:M13021; NID:g160079; PIDN:AAA29485.1; PID:g552179
R;Sjolander, A.; Stahl, S.; Lovgren, K.; Hansson, M.; Cavelier, L.; Walles, A.; Helmby, I
Exp. Parasitol. 76, 134-145, 1393
A;Title: Plasmodium falciparum: the immune response in rabbits to the clustered asparagin A;Reference number: A49245; MUID:93202225; PMID:8454022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cjaccession: T52382
R;Kubo, K.; Sakamoto, A.; Kobayashi, A.; Rybka, Z.; Kanno, Y.; Nakagawa, H.; Nishino, T.
Nucleic Acids Res. 26, 608-615, 1998
A;Title: Cys2/His2 zinc-finger protein family of petunia: evolution and general mechanis: A;Reference number: Z26061
A;Accession: T52382
C;Accession: A23535; A49245
R;Wahlgren, M.; Aslund, L.; Franzen, L.; Sundvall, M.; Wahlin, B.; Berzins, K.; McNicol, Proc. Natl. Acad. Sci. U.S.A. 83, 2677-2681, 1986
A;Title: A Plassmodium falciparum antigen containing clusters of asparagine residues. A;Reference number: A23535; MUID:86206015; PMID:3517875
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C;Species: Petunia x hybrida (garden petunia)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: GB:856699; NID:9298738; PID:9298739
A;Note: sequence extracted from NCBI backbone (NCBIN:127859, NCBIP:127860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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A;Experimental source: strain Mitchell diploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.3%; Score 44; DB 2; Length 451; 50.0%; Pred. No. 1.1e+02; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 477;
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illarity 38.1%; Pred. No. 1.2e+02;
Conservative 5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: November 24, 2004, 09:30:15 Job time: 21.1739 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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A, Residues: 9-25 <$JO>
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Sequence 4, Appli
Sequence 21, Appli
Sequence 37, Appl
Sequence 9, Appli
Sequence 12985, A
Sequence 122185, Sequence 142742,
Sequence 123218,
Sequence 78118,
Sequence 78118,
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                                                                                                                     November 24, 2004, 09:29:11; Search time 82.9783 Seconds (without alignments) 94.040 Million cell updates/sec
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Sequence 4,
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1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-203-942-4
US-10-203-942-4
US-10-203-942-8
US-10-203-942-8
US-10-467-421-21
US-10-336-840-37
US-10-203-942-99
US-10-203-942-99
US-10-424-599-202105
US-10-437-963-123218
US-10-282-122A-78118
US-10-242-599-208738
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Maximum Match 100%
Listing first 45 summaries
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1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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        US-10-424-599-143917
        Sequence 143917, 46.5
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        Sequence 143917, 46.5
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        US-10-437-96-1234-17275
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        Sequence 61375, Ap.
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        App.
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        Sequence 6144, App.
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        Sequence 6123, App.
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        Sequence 6023, App.
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        40.2
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ALIGNMENTS

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APPLICANT: DENOEL, PHILIPPE
APPLICANT: POCLMAN, JAN
APPLICANT: POCLMAN, JAN
APPLICANT: POCLMAN, JAN
PROBLICANT: TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REPRENCE: B45210
CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT APPLICATION NUMBER: PCT/EP01/01556
PRIOR PEPLICATION NUMBER: PCT/EP01/01556
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2000-02-15
PRIOR PRILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PASESEQ FOR Windows Version 4.0
SEQ ID NO 8
LENGTH: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.8%; Score 81.5; DB 14; Length 28; Best Local Similarity 81.8%; Pred. No. 5.7e-05; Matches 18; Conservative 1; Mismatches 0; Indels 3
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Sequence 21, Application US/10467421
Sequence 21, Application US/10467421
Sequence 21, Application US/10467421
GENERAL INFORMATION:
APPLICANT: Berthet, Francois-Xavier Jacques
APPLICANT: Denoel, Philippe
APPLICANT: Poolman, Jan
APPLICANT: Poolman, Jan
APPLICANT: Poolman, Jan
APPLICANT: Thornard, Joelle
TITLE OF INVENTION: Vaccine Composition
FILE REFERENCE: B4529
CURRENT APPLICATION WUMBER: US/10/467,421
CURRENT APPLICATION NUMBER: US/10/467,421
CURRENT FILING DATE: 2003-08-08
PRIOR APPLICATION NUMBER: GB 0103171.5
PRIOR PILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 353
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CTHER INFORMATION: Xaa = Any Amino Acid
US-10-467-421-21
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     APPLICANT: BERTHET, FRANCOIS-XAVIER APPLICANT: DENOEL, PHILIPPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Haemophilus influenzae
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US-10-336-840-37
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Sequence 6, Application US/10203942
| Publication No. US20030096370A1
| GENERAL INFORMATION:
| APPLICANT: BERTHET: FRANCOIS-XAVIER
| APPLICANT: DENOEL, PHILIPPE
| APPLICANT: DOCUMAN, JAN
| APPLICANT: PROCIMAN, JAN
| APPLICANT: PROPERING IN VACCINATION
| TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
| TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
| CURRENT APPLICATION NUMBER: DS. 102-08-15
| PRIOR FILING DATE: 2001-02-13
| PRIOR FILING DATE: 2001-02-13
| PRIOR FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BERTHET, FRANCOIS-XAVIER
APPLICANT: DERTHET, FRANCOIS-XAVIER
APPLICANT: DOCUMAN, DALLIPE
APPLICANT: DOCUMAN, JOELLE
TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN AND USE THEREOF IN VACCINATION
FILE REFERENCE: 845.210
CURRENT APPLICATION NUMBER: US/10/203,942
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR APPLICATION NUMBER: GB 0003502.2
PRIOR FILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-15
SOFTWARE: PRESCO for Windows Version 4.0
SEQ ID NO 4
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 72.8%; Score 81.5; DB 14; Length 19; Best Local Similarity 81.8%; Pred. No. 3.7e-05; Matches 18; Conservative 1; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 112; DB 14; Best Local Similarity 100.0%; Pred. No. 1.9e-09; Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10203942
Publication No. US20030096370A1
GENERAL INFORMATION:
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ORGANISM: Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Haemophilus influenzae US-10-203-942-6
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APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ESEQ ID NO 202105
LENGTH: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.4%; Score 52; DB 14; Length 322; Best Local Similarity 56.5%; Pred. No. 21; Matches 13; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.6%; Score 50; DB 15; Length 101; 38.1%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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US-10-424-599-202105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(101)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                       APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12985
LENGTH: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 202105, Application US/10424599; Publication No. US20040031072A1
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
   HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
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US-10-437-963-142742
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/ US-10-203-942-9

/ Sequence 9, Application US/10203942

/ Sequence 9, Application US/20203942

/ Publication No. US2003009637041

/ GENERAL INFORMATION:
/ APPLICANT: BENDEL, PRANCOIS-XAVIER
/ APPLICANT: DENOEL, PHILIPPE
/ APPLICANT: POOLMAN, JAN
/ APPLICANT: PROPURD: NORELE
/ TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
/ TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
/ TITLE OF INVENTION: HAEMOPHILUS INFLUENCA OUTER MEMBRANE
/ TITLE OF INVENTION NUMBER: PROTICE OUTER
/ PRIOR APPLICATION NUMBER: POT/FP01/01556
/ PRIOR APPLICATION NUMBER: PG 0001562.2
/ PRIOR FILING DATE: 2000-02-15
// RINGRED OF SEQ ID NOS: 9
/ SOFTWARE: FASTESEQ for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 353
/ TUBUST NOTER
/ TERMET: SANDER NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.3%; Score 76.5; DB 14; Length 352; Best Local Similarity 77.3%; Pred. No. 0.0054; Matches 17; Conservative 1; Mismatches 1; Indels 3;
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                       GENERAL INFORMATION:
APPLICANT: TERRY, TANSIN DEBORAH
APPLICANT: TERRY, TANSIN DEBORAH
APPLICANT: HOBB, RHONDA IVY
APPLICANT: DOWNES, JOHN
APPLICANT: DOWNES, MICHAEL PAUL
APPLICANT: DOWNES, MICHAEL PAUL
APPLICANT: DOWNES, MICHAEL PAUL
TILLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
FILE REFERENCE: 37955-0007
CURRENT APPLICATION NUMBER: DCT/AU01/00822
PRIOR APPLICATION NUMBER: PCT/AU01/00822
PRIOR PILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 352
TYPE: PRI
ORGANISM: Haemophilus influenzae
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Publication No. US20030219454A1
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 17; Conserv
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exercise Thomas J
APPLICANT: Annual Constant Constant
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TITLE CONTINGNITION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
FRIOR PILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-06
FRIOR FILING DATE: 2000-05-06
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR FILING DATE: 2000-11-27
FRIOR PAPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-11-27
FRIOR PAPLICATION NUMBER: 60/257,931
FRIOR FILING DATE: 2001-02-09
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Pred. No. 2e+02;
6; Mismatches 6; Indels
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US-10-424-599-208738
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 40.0%;
Matches 8; Conservative (
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                                                     Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
        Zyskind, Judith
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                                                                                                                                                                                                                           Forsyth, R.
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Sequence 12318, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 32 8-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                               APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharow, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 42742
LENGTH: 141
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44.6%; Score 50; DB 16; Length 141;
Best Local Similarity 57.9%; Pred. No. 16;
Matches 11; Conservative 1; Mismatches 7; Indels
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42.9%; Score 48; DB 16; Length 172;
Best Local Similarity 40.9%; Pred. No. 40;
Matches 9; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_43719C.1.pep
US-10-437-963-142742
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US-10-437-963-123218
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
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7 RKVFKMFDKNGDGRITKKELGE 28
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Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
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LENGTH: 172
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
     Sequence 9182, Application US/10739930
Sequence 9182, Application US/20040216190A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLES OF INVENTION: 18-21/33377)
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
SEQ ID NO 9182
LENGTH: 271
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Suguence 61375, Application US/10767701

Suguence 61375, Application US/10767701

Sublication No. US20040172684A1

GENERAL INFORMATION:
APPLICANT: Kovallc, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 61375
LENGTH: 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 41.5%; Score 46.5; DB 17;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSFYDKTSSSSGSDISGLFNPTLHNLG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 9305245.pep
US-10-767-701-61375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 172725, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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13 SPYKGYNRNSTLFNNNIAKSIG 34
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Avoid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 143917
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Publication No. US20040031072A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
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APPLICANT: Anough K
APPLICANT: Anough K
APPLICANT: APPLICANT:
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SEFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 238326
LENGTH: 271
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                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 42.0%; Score 47; DB 15; Length 764; Best Local Similarity 56.2%; Pred. No. 3e+02; Matches 9; Conservative 4; Mismatches 3; Indels
                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_100970C.1.pep
US-10-424-599-143917
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US-10-424-599-238326
     ed. No. 66;
Mismatches
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YSFYDKTSSSGSDISGLFNPTLHNLG 29
     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| ||||||||
714 WNKGSSSNTTSKDWGQ 729
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Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                             175 KNTSQNQSSKNLGE 188
                                                                            9 KNSSSNSTLKNLGE 22
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-143917
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Indels

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Best Local Similarity 55.6%; Pred. No. 1.3e+03;
                                            10; Conservative
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-425-115-297730
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
FILE REPERENCE: ELITAA.034
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-02-23
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-06
PRIOR PELING DATE: 2000-05-06
PRIOR PELING DATE: 2000-05-06
PRIOR PELING DATE: 2000-10-30
PRIOR PELING DATE: 2000-10-30
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2001-10-29
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 172725
LENGTH: 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 16; Length 652;
Pred. No. 3.6e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70833C.1.pep
US-10-437-963-172725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 51602, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zygkind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|| |||:|
169 DYFVYNANSSSS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 DYKLYNKNSSSNS 15
                                                                                                                                                                                                                                                                                               ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-282-122A-51602
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41.1%; Score 46; DB 15; Length 2052;

Query Match

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Sequence 297730, Application US/10425115
; Sequence 297730, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Expu, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; BUMBER OF SEQ ID NOS: 369326
; SEQ ID NO S: 369326
; LENGTH: 71

LENGTH: 71
                                                                                                                                                 Sequence 305355. Application US/10425115

Sequence 305355. Application US/10425115

Sequence 305355. Application No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: Lawid K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yongua
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 305355

LENGTH: 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Clone ID: MRT4577_41553C.1.pep
US-10-425-115-305355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_34603C.1.pep
US-10-425-115-297730
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LOCATION: (1)..(71)
OTHER INFORMATION: unsure at all xaa locations
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Pred. No. 40;
2; Mismatches
                                 : |||| | :|:||
1646 FEKNSSNFSKNTLKNIGD 1663
7 YNKNSS--SNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.2%;
Matches 9; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 YNKNSSSNSTLKNL 20
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SAPELICANT: COUTRERAS, ROLAND HENRI
APPLICANT: CONTRERAS, ROLAND HENRI
APPLICANT: EBERHARDT, INES
APPLICANT: BERHARDT, INES
APPLICANT: BERHARDT, INES
APPLICANT: BUTTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REKGANANS, REKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: WASAT AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT PILING DATE: 2003-06-19
FRIOR PLILING DATE: 2003-06-19
FRIOR PLILING DATE: 2001-12-2
PRIOR PLILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR PLILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: PATENTIN VERSION 3.1
SENDING 13.4
                                                                                                                           APPLICANT: MCCI-Liand, Michael
TITLE OF INVENTION: A METHOD OF IDENTIFYING TARGET ORGANISMS
TITLE OF INVENTION: BY DETERMINING THE CHARACTERISTICS OF THEIR
TITLE OF INVENTION: INTRONIC REGION NUCLEIC ACIDS
FILE REFERENCE: 011399-0005-999
CURRENT APPLICATION NUMBER: US/10/607,559
CURRENT FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US 60/150,977
PRIOR APPLICATION NUMBER: US 60/150,977
PRIOR APPLICATION NUMBER: US 60/150,977
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 225
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Pred. No. 1.5e+02;
3; Mismatches 7; Indels
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40.2%; Score 45; DB 16; Length 338;
Best Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-451-467A-44
Sequence 44, Application US/10451467A
Publication No. US20040161840A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                 Sequence 54, Application US/10607559
Publication No. US20040137463A1
GENERAL INFORMATION:
APPLICANT: Honeycutt, Rhonda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 YKTYTKKASSYTTWKEVSE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 YKLYNKNSSSNSTLKNLGE 22
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Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Tilletia indica
US-10-607-559-54
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                                                                                                                           Sequence 644, Application Us/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Stater, Steven C.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Us/10,369,493

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 6144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Squence 188660, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 188660
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_141374C.1.pep
US-10-424-599-188660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(220)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SDYKL-----YNKNSSSNST 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 YKLYNKNSSSNSTLKNLGE 22
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29 FKLFDKDGNNTMNIKELGE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 36.8
Matches 7; Conservative
47 HNKNKSTNSFLANL
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
US-10-424-599-188660
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LOCATION: (1)..(;
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Gaps

RESULT 24

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Sequence 138, Application US/10451467A

| Sequence 138, Application US/10451467A
| Publication No. US20040161840A1
| GENERAL INFORMATION:
| APPLICANT: CONTEREAS, ROLAND HENRI
| APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
| APPLICANT: REEKMANS, RIERA JOSEPHINA
| APPLICANT: REEKMANS, RIERA JOSEPHINA
| TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
| TITLE OF INVENTION: YEAST AND FUNCI
| FILE REFERENCE: JAB-1667
| CURRENT APPLICATION NUMBER: US/10/451, 467A
| CURRENT APPLICATION NUMBER: EP 00870318.3
| PRIOR APPLICATION NUMBER: EP 01870002.1
| PRIOR FILING DATE: 2001-01-04
| PRIOR FILING DATE: 2001-01-04
| PRIOR FILING DATE: 201-01-04
| PRIOR FILING DATE: 201-01-04
| PRIOR APPLICATION NUMBER: EP 01870003.9
| NUMBER OF SEQ ID NOS: 732
| SOFTWARE: PATENTIN VERSION 3.1
| ENGINE OF SEQ ID NOS: 732
| PRIOR PATENTIN PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.2%; Score 45; DB 15; Length 593; Best Local Similarity 58.8%; Pred. No. 4.5e+02; Matches 10; Conservative 1; Mismatches 6; Indels
                               MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-DEC-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANDEREMATION:
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...593
SEQUENCE DESCRIPTION: SEQ ID NO: 6023:
                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (611)742-4214
INFORMATION FOR SEQ 1D NO: 6023:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 YALVGKNASGKSTLINL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 YKLYNKNSSSNSTLKNL 20
                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserv
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6023, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.2%; Score 45; DB 15;
58.8%; Pred. No. 4.5e+02;
tive 1; Mismatches 6;
                                                                                                                                                                                                                                                                                     STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
NAME/KEY: misc_feature
;
LOCATION: (B) LGCATION 1...589
;
SEQUENCE DESCRIPTION: SEQ ID NO: 6022:
US-10-335-977-6022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REPERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPRAY: (617)227-7400
INFORMATION FOR SEQ ID NO: 6022:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 589 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 YALVGKNASGKSTLINL 392
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 YKLYNKNSSSNSTLKNL 20
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COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.8°
Matches 10; Conservative
                                                                                                                                                                                                                                                                     CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
US-10-335-977-6023
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Congwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brad
APPLICANT: Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Li, Sing
TITLE 
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21(53223) B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT APPLICATION NUMBER: US/10/424,599 NUMBER OF SEQ ID NOS: 285684 SEQ ID NOS: 285684 LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.3%; Score 44; DB 15; Length 51; 64.3%; Pred. No. 40;
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US-10-104-047-3149
US-10-104-04-047-3149
; Sequence 3149, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESERCH INSTITUTE
; FILE OF INVENTION: No. US200330336392A1e1 full length cDNA
; FILE REFERENCE: HI-A01.05
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_87819C.1.pep
US-10-424-599-272204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(51)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 126777, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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15 ENLTKNSFLKNLGE 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 64.3'
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-437-963-126777
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Sequence 279956, Application US/10425115

Fublication No. US2004021427241

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Royalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Caro, Yongue,
APPLICANT: APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (33222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
LENGTH: 92
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40.2%; Score 45; DB 14; Length 1841;
Best Local Similarity 58.8%; Pred. No. 1.6e+03;
Matches 10; Conservative 0; Mismatches 7; Indels (
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39.7%; Score 44.5; DB 17; Length 92;
Best Local Similarity 43.5%; Pred. No. 65;
Matches 10; Conservative 4; Mismatches 4: Indela
                                                                                                                                                                                                                                                                                     Sequence 1341, Application US/10083357
; Publication No. US20030054370A1
; GENERAL INFORMATION:
; AFPLICANT: Qiandong Zeng et al.
; TITLE OF INVENTION: Systemic Discovery of New Genes
; FILE REPERENCE: 032796-090
; CURRENT APPLICATION NUMBER: US/10/083,357
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 1346
; SEQ ID NO 1341
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US-10-425-115-279956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 272204, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION: APPLICANT: La Rosa Thomas J. APPLICANT: Cavalic David K. APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ||:|:||:||
45 FTTYNENHASNTNLDHNTHKNLG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-083-357-1341
                                                                                                                539 YTDYNKNGSSEPRLKTL 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          584 YTDYNKNGSSEPRLKTL 600
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US-10-424-599-272204
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US-10-425-115-279956
                                                                                                                                                                                                                                    RESULT 29
US-10-083-357-1341
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Gaps

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Sequence 116447, Application US/10437963

Sequence 116447, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Each, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Barbaruk, Brad
APPLICANT: Barbaruk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 116447

LENGTH: 256
                                            Gaps
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39.3%; Score 44; DB 16; Length 200;
Best Local Similarity 42.9%; Pred. No. 1.9e+02;
Matches 9; Conservative 6; Mismatches 6; Indels
  39.3%; Score 44; DB 17; Length 159; larity 36.4%; Pred. No. 1.4e+02; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_74470C.1.pep
US-10-437-963-176751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(200)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                   1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                            10 RKVFQMFDKNGDGQITKKELGE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SDYKLYNKNSSSNSTLKNLGE 22
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ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
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ORGANISM: Oryza sativa
FEATURE:
                     Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                          US-10-437-963-176751
    Query Match
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US-10-425-115-221399

Squence 221399, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nocleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53.22)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 221399

LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 62083, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 62083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: MRT4577_133507C.1.pep
US-10-425-115-221399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: Clone ID: 9855880.pep
US-10-767-701-62083
                                                                                                                                                                                                                                                                                           2 SDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                 31 TNVKNVTKLSVSNQTLKDIGE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 NKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:||||:::| ||||
59 NRNSSSSASRKLLGE 73
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3149
LENGTH: 127
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Best Local Similarity 60.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Sorghum bicolor
                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
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US-10-767-701-62083
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139 RNDYKKYGAENTNESTTK 156
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                                                                                                                                                             Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LOWERTON: Anti-Bacterial Vaccine Compositions TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions FILE REFERENCE: 28341/00435; CURRENT APPLICATION NUMBER: US/09/809,665A; CURRENT FILING DATE: 2001-03-15; PRIOR PELICATION NUMBER: 60/123,453; PRIOR FILING DATE: 1999-09-10; PRIOR FILING DATE: 1999-09-10; PRIOR FILING DATE: 1999-04-09; PRIOR FILING DATE: 2000-04-06; NUMBER OF SEQ ID NOS: 197; SEQ ID NOS: 197; SEQ ID NO 153
                                                                                                                                                          Query Match 39.3%; Score 44; DB 16; Length 25 Best Local Similarity 60.0%; Pred. No. 2.5e+02; Matches 9; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                        RESULT 38
US-10-469-93-12
i S-10-469-93-12
i Sequence 12, Application US/10469993
i Publication No. US20040078847A1
i GENERAL INFORMATION:
i APPLICANT: Paldi, Nitzan
i TITLE OF INVENTION:
FILE REFERENCE: 26678
i CURRENT APPLICATION NUMBER: US/10/469,993
i CURRENT FILING DATE: 2003-09-16
i NUMBER OF SEQ ID NOS: 22
i SOFTWARE: Patentin version 3.1
i SEQ ID NO 12
i LENGTH: 368
) NAME/KEY: unsure

; LOCATION: (1)..(256)

; OTHER INFORMATION: unsure at all Xaa locations

; PEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_19948C.1.pep

US-10-437-963-116447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 153, Application US/09809665A Publication No. US20040110268A1 GENERAL INFORMATION:
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177 KVFNKGMSSNSTI 189
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Best Local Similarity 61.5
Matches 8; Conservative
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US-10-469-993-12
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US-09-809-665A-153
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APPLICANT: Holtzman, Douglas
APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Madden, Kevin T.
APPLICANT: Macon, Mary
TITLE OF INVENTION: Mair
TITLE OF INVENTION: Zinc Binuclear Cluster Proteins
FILE REFERENCE: 14184-019US1
CURRENT APPLICATION NUMBER: PCT/US01/29288
PRIOR PLICATION NUMBER: PCT/US01/29288
PRIOR PLICATION NUMBER: PCT/US01/29288
PRIOR PLICATION NUMBER: US 60/233,564
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin Version 3.1
SEQ ID NO 240
LENGTH: 529
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Pred. No. 5.6e+02;
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                                            Sequence 240, Application US/10149310
Publication No. US20040077039A1
GENERAL INFORMATION:
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Best Local Similarity 41.2%;
Matches 7; Conservative
RESULT 40
US-10-149-310-240
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                            November 24, 2004, 09:14:14; Search time 19.3696 Seconds (without alignments) 75.324 Million cell updates/sec
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Sequence
Sequence
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1. /cgn2_6/ptodatca/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodatca/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodatca/1/iaa/6A_COMB.pep:*

3. /cgn2_6/ptodatca/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*

5. /cgn2_6/ptodatca/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Libting first 45 summaries
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1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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44579, A
1, Appli
4, Appli
14158, A
                     22, Appl
3991, Ap
60029, A
19, Appl
33, Appl
30, Appl
1, Appli
1, Appli
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US-09-270-767-43292
Sequence 43292, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
FILE REPRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43292
LENGTH: 482
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-767-58822
| Sequence 58822, Application US/09270767
| Patent No. 6703491
| GENERAL INFORMATION:
| APPLICANT: Homburger et al.
| TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
| FILE REFERENCE: File Reference: 7326-094
| CURRENT APPLICATION NUMBER: US/09/270,767
| CURRENT PILING DATE: 1999-03-17
| NUMBER OF SEQ ID NOS: 62517
| SEQ ID NO 58822
| LENGTH: 219
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Sequence 4
Sequence 1
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PCT - USS5 - 09641 - 4
PCT - USS6 - 07709 - 22
US - 09 - 270 - 767 - 6029
PCT - USS6 - 07709 - 19
PCT - USS6 - 07709 - 33
PCT - USS6 - 07709 - 32
US - 09 - 541 - 755 - 1
US - 09 - 134 - 000C - 4344
US - 09 - 270 - 767 - 44579
US - 09 - 213 - 2930 - 1
US - 09 - 213 - 2930 - 1
US - 09 - 213 - 694A - 4
US - 09 - 527 - 084A - 4
US - 09 - 527 - 084A - 4
US - 09 - 248 - 796A - 14158
US - 09 - 248 - 796A - 23261
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Pred. No. 4.3;
3; Mismatches
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101 RLNYKLFLCRNSSQSTLKN 119
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Best Local Similarity 57.9%;
Matches 11; Conservative
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Sequence 4703491

Patent No. 6703491

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 44496

LENGTH: 300
                                                                                                            GENERAL INFORMATION:
APPLICANT Homburger et al.
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37611
LENGTH: 179
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Sequence 52828, Application US/09270767
Sequence 52828, Application US/09270767
Reacht No. 6703491
SEGUENT NO. 6703491
STITLE OF INVENTION:
PILLE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 52828
LENGTH: 179
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50.0%; Pred. No. 14;
tive 3; Mismatches 5; Indels
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                                                              Sequence 37611, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
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Best Local Similarity 50.03
Matches 8; Conservative
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Best Local Similarity 50.0
Matches 8; Conservative
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                                                JS-09-270-767-37611
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Sequence 1721, Application US/09248796A

Sequence 1721, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17231
LENGTH: 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27899, Application US/09248796A
| Sequence 27899, Application US/09248796A
| Patent No. 6747137
| GENERAL INFORMATION:
| APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
| TITLE OF INVENTION: NUMBER: US/09/248,796A
| CURRENT APPLICATION NUMBER: US 60/074,725
| PRIOR APPLICATION NUMBER: US 60/074,725
| PRIOR FILING DATE: 1998-02-13
| PRIOR FILING DATE: 1998-08-13
| NUMBER OF SEQ ID NOS: 28208
| SEQ ID NO 27899
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.. OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-7968-27899
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                          2; Indels
1 Similarity 64.7%; Pred. No. 32;
11; Conservative 2; Mismatches
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                                                                                                133 SDYNI --KNSSNNPTLK 147
                                                                      2 SDYKLYNKNSSSNSTLK 18
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Candida albicans
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Best Local Similarity
2, Conserve
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Best Local Similarity
Matches 9; Conserva
  Best Local Similarity
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                                                                                                                                                                                                                US-09-248-796A-17231
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                          Matches
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US-09-248-796A-15815

i Sequence 15815, Application US/09248796A

j Patent No. 6747137

GENERAL INFORMATION:

i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

i TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.13

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 15815

LENGTH: 249

LENGTH: 249
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                             APPLICANT: CLARITY BIOSCIENCES, INC.
APPLICANT: Honeycutt, Rhonda
APPLICANT: HONEYCUTT, Rhonda
APPLICANT: HONEYCUTT, Rhonda
APPLICANT: MCCLELLand, Michael
TITLE OF INVENTION: IDENTIFYING ORGANISMS BY DETECTING
TITLE OF INVENTION: INTRONIC NUCLEIC ACIDS OR ENCODED PROTEINS
TITLE OF INVENTION: INTRONIC NUCLEIC ACIDS OR ENCODED PROTEINS
TITLE OF INVENTION UNMBER: US 09/645,055
CURRENT APPLICATION NUMBER: US 60/150,977
PRIOR APPLICATION NUMBER: US 60/150,977
PRIOR APPLICATION NUMBER: US 60/150,977
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45;
Pred. No.
                                                                                  Sequence 54, Application US/09645055
Patent No. 6599701
GENERAL INFORMATION:
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24 IYNNNNSNSKTYKNI 38
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Best Local Similarity 47.4%
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Tilletia indica
US-09-645-055-54
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Best Local Similarity
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US-09-248-796A-15815
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                                                             13-09-645-055-54
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i Sequence 21631, Application US/09248796A

i Patent No. 6747137

i GENERAL INFORMATION:

A PAPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-13

PRIOR PILING DATE: 1999-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 21631

LENGTH: 159

LENGTH: 159
                                                                                                                                                                                                                                                                                                                                             US-09-543-681A-4823
US-09-543-681A-4823
Sequence 4823, Application US/09543681A
Fatent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
FRIOR FILING DATE: 199-04-09
PRIOR FILING DATE: 199-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4823
LENGTH: 60
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                                                                                                                           Query Match
41.1%; Score 46; DB 4; Length 300;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 5; Indels
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Pred. No. 18;
5; Mismatches 6; Indels
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                                                      ) OTHER INFORMATION: Xaa means any amino acid US-09-270-767-44496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | | : | : | | : | 136 KKDYKKSHTNNNSNSNVNN 154
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                                                                                                                                                                                                                    1 RSDYKLYNKNSSSNST 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Proteus mirabilis US-09-543-681A-4823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans
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Best Local Similarity 42.1
Matches 8; Conservative
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Best Local Similarity
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                                             FEATURE:
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j Sequence 2, Application US/08850917
j Sequence 2, Application US/08850917
j Patent No. 5854045
j GENERAL INFORMATION:
j APPLICANT: Hangiusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
j CORRESPONDENCE ADDRESS:
j ADDRESSEE: Klauber & Jackson
j STRET: All Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.7%; Score 44.5; DB 1; Length 1237; 52.4%; Pred. No. 2.4e+02;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION NUMBER: US/08/850,917
FILING APPLICATION NUMBER: US/08/850,917
FILING APPLICATION NUMBER: US/08/850,917
APPLICATION NUMBER: US/08/21,853
FILING DATE: 12-MAY-1994
ATTONNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELEPHONE: 201487-5800
                                                                      SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,853
FILING DATE: US-MAY-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: Jackson Esq., 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELEPRANICATION INPORMATION:
TELEPRANICATION INPORMATION:
TELEPRANICATION 1487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 DY-KLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Gallus domesticus
                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1237 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 52.49
Matches 11, Conservative
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TELEX: 133521
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TOPOLOGY: linear
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US-08-850-917-2
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| Sequence 590, Application US/09538092
| Patent No. 6753314
| GENERAL INFORMATION:
| APPLICANT: Glot, Loi:
| APPLICANT: Mansfield, Traci A. |
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-54
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-54
| FILE REFERENCE: 15966-54
| CURRENT APPLICATION NUMBER: 60/127,352
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 2000-02-01
| PRIOR FILING DATE: 2000-02-01
| NUMBER OF SEQ ID NOS: 1387
| SEQ ID NO 590
| LENGTH: 1382
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Sequence 2, Application US/08241853
Sequence 2, Application US/08241853
SERENT NO. 569348
SERENT INFORMATION:
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 40.2%; Score 45; DB 4; Length 1382; Best Local Similarity 58.8%; Pred. No. 2.3e+02; Matches 10; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                Query Match 40.2%; Score 45; DB 4; Length 733; Best Local Similarity 41.2%; Pred. No. 1.1e+02; Matches 7; Conservative 6; Mismatches 4; Indels
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YLR466W
US-09-538-092-590
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5599
LENGTH: 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5599
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                                                                                                                                                                                                                                                                                                                                                                          1 RSDYKLYNKNSSSNSTL 17
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1 RQDFKLMNQNTNTEDTI 17
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COMPUTER READABLE FORM:
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US-09-538-092-590
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Gaps

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Sequence 17634, Application US/09248796A

Requence 17634, Application US/09248796A

Requence 17634, Application US/09248796A

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WINDER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-06-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17634
                                                                                                                                               Sequence 47374, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:

TITLE OF INVENTION: NUMBER: US/09/270,767

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62217

SOUTWARE: Patentin Ver. 2.0

SEQ ID NO 47374

LENGTH: 213

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-47374
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Patent No. 6790950
GENERAL INFORMATION.
APPLICANT: Lowery B., David, et al.
TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REFERENCE: 28941/00435
CURRENT APPLICATION NUMBER: US/09/809,665A
CURRENT FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.3%; Score 44; DB 4; 38.1%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 4;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 TDYNIYNKYHSNNNFNKKTNQ 28
2 SDYKLYNKNSSSNSTLKNLGE 22
                         2 SDYKLYNKNSSSNSTLKNLGE 22
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 36.1.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-248-796A-17634
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Sequence 2650, Application US/09248796A

Sequence 2650, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: WUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26540

LENGTH: 72
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Ratent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburer et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32157
LENGTH: 213
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                                                                                                                                                                                                                                        39.7%; Score 44.5; DB 2; Length 1237; 52.4%; Pred. No. 2.4e+02; tive 3; Mismatches 6; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 39.3%; Score 44; DB 4; Length 72; Local Similarity 50.0%; Pred. No. 10; nes 10; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                              151 DYGNIEEKNNSAEVTLKNLKE 171
                                                                                                                                                                                                                                                                                                                                     3 DY-KLYNKNSSSNSTLKNLGE 22
                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
CRGANISM: Gallus domesticus
STRAIN: DT40
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; ORGANISM: Drosophila melanogaster
US-09-270-767-32157
                  SEQUENCE CHARACTERISTICS:
LENGTH: 1237 amino acids
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Matches 8; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local $
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US-09-134-000C-6579
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                                                            TYPE: PRT
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| Patent No. 6617156
| Patent No. 6617156
| GENERAL INPORMATION:
| APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: BUTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: BUTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 032796-032
| CURRENT APPLICATION NUMBER: US 60/055,778
| PRIOR APPLICATION NUMBER: US 60/055,778
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
SOFTWARE: PRIOR FILING 31
SEQ ID NOS: 6812
SOFTWARE: PRIOR DATE: PRIOR DATE
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, OTHER INFORMATION: Amino acid 15 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-4078
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45.0%; Pred. No. 22;
tive 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.3%; Score 44; DB 4; Length 369; ilarity 44.4%; Pred. No. 70; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Actinobacillus pleuropneumoniae
PRIOR APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/128,689
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-06
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 153
LENGTH: 369
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Matches 8; Conserv
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Sequence 6679, Application US/09134000C

Sequence 6679, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: ENTEROCCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ENTEROCCCUS FACALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US/09/134,000C

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NOS: 6812

SEQ ID NO 6679

LENGTH: 214
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 78
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                                                                            Query Match 38.8%; Score 43.5; DB 4; Length 214; Best Local Similarity 45.0%; Pred. No. 44; Matches 9; Conservative 6; Mismatches 4; Indels 1
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38.4%; Score 43; DB
Best Local Similarity 44.4%; Pred. No. 16;
Matches 8; Conservative 5; Mismatches
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                                                                                                                                                                                                                   192 YKVTFNEESKKFTTIENLGE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 YKVTFNEESKKFTTIENLGB 211
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                                                                                                                                                                                   4 YKL-YNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 YKL-YNKNSSSNSTLKNLGE 22
ORGANISM: Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
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Best Local Similarity
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IMMUNOCONJUGATES AND HUMANIZED
ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
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                                                               Gaps
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US-09-155-107-4
Sequence 4, Application US/09155107
Patent No. 6254868
GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, HANS
APPLICANT: QU, Zhengxing
TITLE OF INVENTION: GLYCOSYLATED HUMANIZED B-CELL SPECIFIC ANTIBODIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
             Score 43; DB 1; Length 116;
Pred. No. 26;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.4%; Score 43; DB 3; Length 116; 47.1%; Pred. No. 26; tive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRASSES:
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
CONNTRY: USA
ZIP: 20007-5109
COMPUTER: USA
COMPUTER: FROABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICEATION DATA:
APPLICATION NUMBER: US 08/690,102
FILING DATE: 01-701-1996
APPLICATION NUMBER: US 08/289,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, BETNARD D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/463/IMIN
TELECHONE: (202)672-5300
TELECHONE: (202)672-5300
                                                                                                                                                                                                                                                     Sequence 4, Application US/09127902
| Patent No. 6187287
| GENERAL INFORMATION:
| APPLICANT: LEUNG, Shui-on
| APPLICANT: HANSEN, HANS
| TITLE OF INVENTION: INVINDOIES SPINDINGES:
| NUMBER OF SEQUENCES: 21
| CORRESPONDENCE ADDRESS:
                                                                                                      1 RSDYKLYNKNSSSNSTL 17
                                                                                                                                     54 RNDYTEYNONFKDKATL 70
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                  38.4%;
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Query Match
Best Local Similarity 47.1*
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 47.1
Matches 8; Conservative
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MOLECULE TYPE: protein
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CLASSIFICATION:
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Patent No. 5789554

GENERAL INFORMATION:
APPLICANT: LEUNG, Shui-on
APPLICANT: HANSEN, Hans
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                             Sequence 49247, Application US/09270767
Fatent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
LENGTH: 78
LENGTH: 78
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Pred. No. 16;
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CUUTY: WASAINIGCON, D.C.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/690,102A
FILING DATE: 01-JUL-1996
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/899,576
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE: BETHAND A.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18,655
REFERENCE/DOCKET NUMBER: 18,655
REFERENCE/DOCKET NUMBER: 18,655
REFERENCE/DOCKET NUMBER: 18,655
REFERENCE/DOCKET NUMBER: 18,733/463/IMIN
TELECOMMUNICATION: NONDARIAND: 10,70,1679_2670
                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SDYKLYNKNSSSNSTLKN 19
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(202) 672-5399
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-690-102A-4
               RESULT 25
US-09-270-767-49247
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Aguence 3991, Application US/09583110

j Sequence 3991, Application US/09583110

j Patent No. 6699703

j GENERAL INFORMATION:

j TITLE OF INVENTION:

j PRIOR APPLICATION NUMBER: US/09/583,110

j PRIOR FILING DATE: 1998-06-30

j PRIOR FILING DATE: 1998-06-30

j PRIOR FILING DATE: 1998-05-12

j PRIOR FILING DATE: 1998-05-12

j PRIOR FILING DATE: 1997-07-02

j RIOR FILING DATE: 1997-07-02

j RIOR FILING DATE: 1998-05-12

j RIOR FILING DATE: 1998-05-12
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38.4%; Score 43; DB 4; Length 185;
Best Local Similarity 47.4%; Pred. No. 44;
Matches 9; Conservative 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PELLOATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 5;
Pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REPERRICE/DOCKET NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-0223
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 60029, Application US/09270767; Patent No. 6703491
                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 KLYENNPSNNMTWKVAGQ 146
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Best Local Similarity 50.0%;
Matches 9; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
Colorado
                            U.S.A.
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US-09-270-767-60029
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TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR B-CELL LYMPHOMA AND LEUKEMIA CELLS
NUMBER OF SEQUENCES: 21
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: DCT/US95/09641
FILING DATE: 11-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,576
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38.4%; Score 43; DB 3; Length 116;
Best Local Similarity 47.1%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches 6; Indels
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APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                CURRENT APPLICATION NUMBER: US/09/155,107
CURRENT FILING DATE: 1998-11-17
EARLIER PELING DATE: 1998-11-17
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
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STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US96-07709-22; Sequence 22, Application PC/TUS9607709; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9509641
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RSDYKLYNKNSSSNSTL 17
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54 RNDYTEYNQNFKDKATL 70
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
FILE REFERENCE: 018733/0879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Murine
US-09-155-107-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US95-09641-4
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PCT-US96-07709-33
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                 APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster TITLE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                      Query Match 38.4%; Score 43; DB 4; Length 195; Best Local Similarity 57.1%; Pred. No. 47; Matches 8; Conservative 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tripp, Cynthia A.
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisnewski, Mancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLAN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US96-07709-19; Sequence 19, Application PC/TUS9607709; GENERAL INFORMATION:
                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-60029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFRENCE/DOCKET NUMBER: 2618-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-0700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 KLYENNPSNNMTWKVAGO 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 197 amino acids
amino acid
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Best Local Similarity 50.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
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CITY: Denver
STATE: Colorad
                                                                                                                                                                                       SEQ ID NO 60029
LENGTH: 195
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RESULT 34

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Gaps
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Pred. No. 50;
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GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ANDERSS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
Sequence 33, Application PC/TUS9607109
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCES: 43
CORRESPONDENCES: Aberidan Rose & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-130-PCT
TELECOMMULICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFRAX: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PELLATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 KLYENNPŚNNMTWKVAGO 130
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50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                           U.S.A.
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CLASSIFICATION:
                                                                                                                                                                                                                                                       CITY: Denver
STATE: Colora
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                             80203
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amino acid
                Best Local Similarity
Matches 8; Conserv
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STATE: Colora
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US-09-134-000C-4344
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ZIP: 80203
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lustigman, Sara
APPLICANT: Destiman, Eric
APPLICANT: Destiman, Eric
APPLICANT: Unnasch, Thomas
TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
FILE REFERENCE: 6475/252
CURRENT APPLICATION NUMBER: US/09/541,759
CURRENT PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 1.
LENGTH: 223
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Sequence 44586, Application US/09270767

Sequence 46703491

Sequence 4703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION:

TITLE REFERENCE: File Reference: 7326-094

CURRENT PLLING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 44586

LENGTH: 244
                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 54;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44586
                                                          2618-30-PCT
                NAME: Connell, Gary J.

REGISTRATION NUMBER: 2618-
REFERENCE/DOCKET NUMBER: 2618-
TELECOMMUNICATION INFORMATION:
TELEPRONE: (303) 863-9700
TELEPRAX: (303) 863-9700
TELEPRAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
TYPE: TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-07709-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09541759
Patent No. 6723322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                129 KLYENNPSNNMTWKVAGQ 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| | |:| | |:
129 KLYENNPSNNMTWKVAGQ 146
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Onchocerca volvulus
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
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Patent No. 6617156

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FACCALIS FOR DIAGNOSTICS AND THERAPEUTICS;
TITLE OF INVENTION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
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Score 43; DB 4; Length 244;
Pred. No. 61;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                   PCT-US96-07709-25

Sequence 25, Application PC/TUS9607709

GENERAL INFORMATION:
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPEN: (303) 863-9700
TELEFEN: (303) 863-9700
TELEFEN: (303) 863-0223
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 KLYENNPSNNMTWKVAGQ 174
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  38.4%;
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                                                                                                                              100 YNLYAKNNNSNS 111
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Matches 9; Conservative
                                                    Conservative
                                                                                                4 YKLYNKNSSSNS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-270-767-44579

Sequence 44579, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTING DATE: 2.0

SEQ ID NO 44579

LENGTH: 307
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                                                                                                                               Query Match
38.4%; Score 43; DB 4; Length 281;
Best Local Similarity 62.5%; Pred. No. 73;
Matches 10; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.4%; Score 43; DB 4; Length 307; Best Local Similarity 57.1%; Pred. No. 80; Matches 8; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 24, 2004, 09:31:39 Job time: 21.3696 BecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44579
; SEQ ID NO 4344
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4344
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246 RSDWKDYLYNVNKSNN 261
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Plasmodiu

Streptoco Helicobac H. pylori Novel hum Acinetoba Drosophil Human sec Protein s Disease t S. cerevi Yeast smO Chicken p

Novel hum

Abu23678
Adf64538
Adf64538
Adse30847
Abg93043
Abw20085
Aaw20085
Aaw20085
Abb71161
Adb32893
Abr52794
Ab

us-09-719-379a-2.rag

Seguence:

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Run ž

Searched:

Database

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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae, Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79953, and AAZ91201 to AAZ31252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine, non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; llipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; onjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-typeable H. influenzae 1715MEE Group 2a type peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                ABU23678
ADF04538
ADF04538
ADF04538
AAE30847
ABG93043
AAW20085
AAW20085
AAW20085
AAW201461
ADA34312
ABB71161
ADA34312
ABB71161
ADA34312
ABB71161
ADA34312
ABB71283
ABW52164
ABW52164
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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                                                                                                                                                          Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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Haemophilus influenza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Hemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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Lobet Y;

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Gaps

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Indels

Length 22;

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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                            The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein PS; (MOMP PS) of non-typeable H. influenzae (ntHi). Each of these peptides contain an LBI(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP PS from strain ntHill28, representing amino acids Argl17 to Glyl35. This peptide represents the third exposed loop of PS and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Heemophilus
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                                                             Recombinant bacterial outer membrane protein where one or more surface exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                      influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 112; DB 4;
100.0%; Pred. No. 2.9e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSDYKLYNKNSSSNSTLKNLGE 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY79993 standard; protein; 464 AA
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(OHIS ) UNIV OHIO STATE RES FOUND
                                                                                                                                                                          Claim 2; Page 26; 29pp; English.
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                                                                                                                               media and conjunctivitis.
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Best Local Similarity 100.
Matches 22; Conservative
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                    WPI; 2001-522599/57
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                                                                                                                                                                                                                                                                                                     Recombinant bacterial outer membrane protein where one or more surface-
exposed loops are modified is useful as a vaccine to prevent or treat
Haemophilus influenzae infection or associated disease, e.g., otitis
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not-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
otitis medala; sinusitis; conjunctivitis;
lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
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                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
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                                                                                    13-FEB-2001; 2001WO-EP001556
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22; Conservative
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WO200161013-A1
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Best Local Similarity
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                                               otitis media, sinusitis, conjunctivitis, or lower respiratory, react infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAV79955 to AAY79993, and AAS91201 to AAZ91252, represent sequences used in the exemplification of the present invention
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                                        aB
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            peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such
                                                                                                                                                                                              Gaps
 present invention describes antigenic P5-like fimbrin subunit
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                                                                                                                                                                      Length 464;
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                                                                                                                                                                    100.0%; Score 112; DB 3; 100.0%; Pred. No. 7.5e-09;
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                                                                                                                                                                                                                                       377 RSDYKLYNKNSSSNSTLKNLGE 398
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                                                                                                                                                                                             22, Conservative
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Best Local Similarity
                                                                                                                                             Sequence 464 AA;
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Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptides (IBI(f) peptides) of P5-like fimbrin proteins from various peptides (IBI(f) peptides) of P5-like fimbrin proteins from various prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influenzae, Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAV79955 to AAV79931, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Hamophilus influenzae; PS-like fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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95.5%; Pred. No. 3.5e-08;
tive 0; Mismatches 0;
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                                                                          RSDYKLYNKN-SSNSTLKNLGE
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les 21; Conserv
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Matches
    Matches
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ID AAY7
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AC AAY7
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine, non-typeable Haemophilus influenzae, ntHi, infection, chimeric protein, Haemophilus influenzae, P5-like fimbrin protein, lipoprotein D; LB1(f), immunogenic, antigenic, otitis media, sinusitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-typeable H. influenzae group 2 LB1(f) peptide N1236MBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.4e-06;
2; Mismatches 0; Indels
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81.8%; Pred. No. 6.4e-06;
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                                                                                                                                                         Lobet
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                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                       Dequesne G,
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                                                                                                                                                                                                                                                                                               Example 1; Page 30; 68pp; English
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                    99WO-US011980
                                                         98GB-00012613
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(OHIS ) UNIV OHIO STATE
                                                                                                                                                           Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bakaletz LO, Cohen J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
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                  28-MAY-1999;
                                                           11-JUN-1998;
                                                                                                                                                         Bakaletz LO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. Influenzae and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
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                                                                           Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Hemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                    Non-typeable H. influenzae group 2 LB1(f) peptide NTHI-502.
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(first entry)
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                                                                                                                                                                              Haemophilus influenzae
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Best Local Similarity
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ID AAB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                               otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influenzea. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAV79955 to AAY79993, and AAS91201 to AAA291252, represent sequences used in the exemplification of the present invention
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                                             peptides (LBI(f) peptides) of PS-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections such offices, sinualitis, conjunctivitis, or lower respiratory tract
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                                    present invention describes antigenic P5-like fimbrin subunit
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                                                                                                                                                                                                   J. Length 19;
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                                                                                                                                                                                                Score 81.5; DB 3
Pred. No. 1e-05;
1; Mismatches
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                                                                                                                                                                                                                                                                1 RSDYKLYNKNS---STLKDLGE 19
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          Example 1; Page 30; 68pp; English
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                                                                                                                                                                                                  72.8%;
81.8%;
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                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Matches 18; Conserva
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                                                                                                                                                                          Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                         Gaps
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         Length 19;
                                                           Indels
                                                           ö
       Score 81.5; DB 3;
Pred. No. 1e-05;
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                                                         Mismatches
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                                                                                                                                                       RSDYKLYNKNS---STLKDLGE 19
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         72.8%;
81.8%;
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Best Local Similarity 81.8
Matches 18; Conservative
                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-116457/10
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9964067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein PS (MOMP PS) of non-typeable H. influenzae (ntHi). Each of these peptides contain an LBI(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP PS from strain ntHill28, representing amino acids Argl17 to G1y13. This peptide represents the third exposed loop of PS and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Haemophilus sinfluenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
                                                                                                                                                                                                                                                                                                                      Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface exposed loop; major outer membrane protein P5; MOMP P5; non-typeable H. influenzae; ntH1; LB1(f) peptide; B cell epitope; otitis media; sinusitis; conjunctivitis;
                                                                            surface exposed loop; major outer membrane protein P5; MOMP P5;
on-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
othtis media; sinustitis; conjunctivitis;
lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                                                      peptide from strain ntHi-183NP (Group 2b type).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entire 3rd loop from strain ntHi-183NP (Group 2b type).
                                                                                                                                                                                                                                                                           Denoel P, Poolman J, Thonnard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.8%; Score 81.5; DB 4
81.8%; Pred. No. 1e-05;
ive 1; Mismatches
                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSDYKLYNKNS---STLKDLGE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB47446 standard; peptide; 28
                                                                                                                                                                                                       13-FEB-2001; 2001WO-EP001556.
                                                                                                                                                                                                                              15-FEB-2000; 2000GB-00003502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                           media and conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                     Haemophilus influenzae
                                                                                                                                                                                                                                                                                                  WPI; 2001-522599/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 AA;
                                                                                                                                                           WO200161013-A1.
                                                      LB1(f) cont.
                                                                                                                                                                                                                                                                           FJ,
                                31-OCT-2001
                                                                                                                                                                                  23-AUG-2001
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          AAB47442;
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                                                                                                                                                                                                                                                                            Berthet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein Ps (MOMP Ps) of non-typeable H. influenzae (ntill). Each of these peptides contain an LB1(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP Ps from strain ntHill28, representing amino acids Argl17 to Gly135. This peptide represents the third exposed loop of Ps and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP Ps may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., ottis media, sinusitis, conjunctivitis, or lower respiratory tract infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hyperblebbing; Gram-negative bacterium; genetically modified; Tol gene; peptidoglycan-binding; peptidoglycan-associated slte; outer-membrane; bacterial infection; vesicle-shedding; Bleb; filter sterilised; detergent; deoxycholate; homogeneity; antibacterial; vaccine; HiRD; PS; P6; PCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.8%; Score 81.5; DB 4; Length 28; 81.8%; Pred. No. 1.6e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Poolman J, Thonnard J;
                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG80420 standard; protein; 353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae P5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2001; 2001GB-00003171.
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                                                                                                                                                                                                13-FEB-2001; 2001WO-EP001556.
                                                                                                                                                                                                                                                                 15-FEB-2000; 2000GB-00003502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deery Match
Best Local Similarity 81.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  media and conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                Berthet FJ, Denoel P,
Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-522599/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200262378-A2.
                                                                 WO200161013-A1
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                                                                                                                                  23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG80420
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AAY79980;
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                                                                                                                                                                The present invention relates to a new hyperblebbing Gram-negative bacterium genetically modified by one or more processes selected from down-regulating expression of one or more Tol genes and attenuating the peptidoglycan-binding activity by mutation of one or more gene(s) encoding a protein comprising a peptidoglycan-associated site. The invention is useful in a method of treatment of the human or animal body. The invention is also useful for protecting an individual against a bacterial infection. The invention has improved outer-membrane vesicles shedding properties. Blebs are more easily made in higher yield from the invention, and are more hongeneous in nature and can be more readily filter sterilised. The blebs can be made and harvested without the use of detergents such as deoxycholate, thus obviating chromatography filter sterilised. The blebs to be made and harvested from the invention have reduced particle size (allowing sterile filtration through 0.22 mum pores), increased batch honogeneity, and a superior yield. The present amino acid sequence represents a Haemophilus influenzae protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                            Novel hyperblebbing Gram-negative bacterium that has been genetically modified by down-regulating expression of Tol genes, and/or attenuating peptidoglycan-binding activity useful for treating bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface exposed loop; major outer membrane protein P5; MOMP P5;
on-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
ottiis media; sinustiis; conjunctivitis;
lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                            72.8%; Score 81.5; DB 5; Length 353;
81.8%; Pred. No. 0.00035;
cive 1; Mismatches 0; Indels
                                   Thonnard J;
                                   Neyt CA, Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Loop 4
/note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38. .57
/label= Loop 1
/note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99. .100
|label= Loop 2
note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= Loop 3
'note= "Extracellular domain"
            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 RSDYKLYNKNS---STLKDLGE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                             Disclosure; Page 58; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB47447 standard; protein; 353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .204
                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
                                   Denoel P,
                                                          2002-657509/70.
                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                      N-PSDB; ABS66193
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 353 AA;
                                   FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB47447;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                   Berthet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOMP P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
AAB47447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
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                                                                                                                                                                                                                                                                                                                                                             Poolman J, Thonnard J;
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                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 RSDYKLYNENS---STLKKLGE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY79980 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1, 29pp, English.
                                                                                                                                        13-FEB-2001; 2001WO-EP001556.
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                                                                                                                                                                                                                    15-FEB-2000; 2000GB-00003502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               media and conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                 Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-522599/57
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 353 AA;
WO200161013-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                 Berthet FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1999
                                                                    23-AUG-2001
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the 6213 antiense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a promoter operably linked to the mucleic acid comprising a promoter operably linked to the mucleic acid containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular containing the polypeptide; (7) identifying a gene in an operon required for proliferation, or that has an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation or the activity of compound that influences the activity of identifying a gene required for cellular proliferation of the pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the tearget of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation of sereening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation to isolate candidate molecules for rational confident did not form pate of the present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this paternal of the prince of specification, of the present sequence is encoded by one of the present of the present sequence agains of the present of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 42.9%; Score 48; DB 6; Length 706; Similarity 40.0%; Pred. No. 1.5e+02; 8; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermococcus kodakaraensis KOD1 protein sequence SeqID848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN46970 standard; protein; 1390 AA.
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DYERFNVNKASNTVLSSLNQ 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2003; 2003WO-IB003597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-AUG-2002; 2002JP-00319011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-257583/24
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 706 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                              Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                   The present invention describes antigenic PS-like fimbrin subunit peptides (LB1(f) peptides) of PS-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.9%; Score 76; DB 3; Length 20; 77.3%; Pred. No. 8.1e-05;
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tches 3; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #35721.
                                Lobet Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSDYKLYNKNSSSNSTLKNLGE 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABUS0194 standard; protein; 706 AA
                                                                                                                                                                         Example 1; Page 30; 68pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072861.
06-MAR-2002; 2002US-0362699P.
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                              Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zamudio C,
Trawick JD,
                                                                     WPI; 2000-116457/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20 AA;
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                              Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002
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Wall D,
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This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential date of the genome of such organism, selecting at least a rebitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, contains a sequence homologous with the selected region and amaker gene, contains a contains a sequence homologous recombination. The genome is preferably the genome of a hyperthermostable archabacterium, particularly the genome of a paper in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of concoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the concoded by the genome of Thermococcus kodakaraensis which was derived efficiently and reliably. The present sequence is that of a protein encoded by the genome of Thermococcus kodakaraensis which was derived efficiently and reliably. The present sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the present sequences.

It is electronic format directly from WIPO at the print was obtained the without and part of the printed specification, but was obtained the was obtained the print was obtained the pr
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  Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%; Score 48; DB 8; Length 1390; 38.5%; Pred. No. 3.4e+02; Live 7; Mismatches 5; Indels
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                                                                                                    Claim 9; SEQ ID NO 848; 598pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSDYK----LYNKNSSSNSTLKNLGE 22
                                                    studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB61852 standard; protein; 1878 AA
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11-JUL-2000; 2000US-00614150.
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Matches 10; Conserva
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The invention relates to a novel urinary specific nucleic acid molecule (USNA). A protein encoded by a USNA of the invention has cytostatic activity. The USNA may have a use in gene therapy, and as a vaccine.

These nucleic acids and polypeptides are also useful for diagnosing and monitoring the presence and metastases of urinary cancer in a patient. The artibody that specifically binds to the lung specific polypeptide is useful for determining the presence of a urinary specific protein in a sample, as well as for treating a patient with cancer, particularly by inducing an immune response against the urinary cancer cell expressing the urinary specific genes and proteins are useful for identifying, these urinary specific genes and proteins are useful for identifying, diagnosing, monitoring, teaging, imaging and treating urinary cancer (e.g. squamous cell carcinoma) and non-cancerous disease states in the urinary. The sequences shown in ADD71534-ADD71716 represent urinary
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           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence (ABL16176-ABL30511), between the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New urinary specific genes and proteins, useful in gene therapy or as vaccines for treating urinary cancer or non-cancerous urinary diseases, as well as for diagnosing, monitoring or staging such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; urinary specific nucleic acid; USNA; cytostatic; gene therapy; vaccine; urinary cancer; urinary specific protein; USP; cancer; squamous cell carcinoma.
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                                                                                                                                                                                                                                                                                             Length 1878;
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45.0%; Pred. No. 4.9e+02;
Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human urinary specific protein sequence SEQ ID NO:420.
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nes 9; Conserv
                                                                                                                                                                                                                                                     Sequence 1878 AA;
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Protein identification; aignal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                  Gaps
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Length 510;
Score 47; DB 2; Length 510 Pred. No. 1.5e+02; 9; Mismatches 3; Indels
                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 38230.
                                                                                                                                                                                 AAG31785 standard; protein; 324 AA
                                                                                   103 KTNFQVYQKGHNSNTTLKD 121
                                                                1 RSDYKLYNKNSSSNSTLKN 19
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99US-0123180P.
99US-0125784P.
99US-0126564P.
99US-0126785P.
99US-0126785P.
99US-0128744P.
99US-0138077P.
99US-0131849P.
99US-0131849P.
99US-0131849P.
99US-0131848P.
99US-013248P.
99US-013248FSP.
99US-013248FSP.
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99US-013248FSP.
99US-013248FSP.
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99US-0135124P.
99US-0135353P.
99US-0135629P.
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99US-0134221P.
99US-0134370P.
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99US-0138540P.
99US-0138847P.
 42.0%;
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99US-0136782P
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                                                                                                                                                                                                                                                  17-OCT-2000 (first entry)
 Query Match
Best Local Similarity 36.8
Matches , 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
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09-MAR-1999
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                                                                                                                                                  RESULT 24
                                                                                                                                                                                                  셤
                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a cytochrome P450 protein, CYP94A6, of tobacco that is expected to have fatty acid hydroxylase activity since is displays the characteristic signature motif for this class of enzymes.

The invention provides isolated mucleic acids (see AAX58400-06) encoding plant fatty acid hydroxylases (see AAY05896-902). Also claimed are host cells, transpenic plants and compositions consisting of the plant fatty acid hydroxylase genes from a plant, and a process of altering fatty acid hydroxylase genes from a plant, and a process of altering fatty acid hydroxylase genes from a plant by expressing the plant fatty acid dydroxylase in a plant by expressing the plant fatty acid dydroxylase in a plant by expressing the plant fatty acid content composition in a plant by expressing the hydroxylated fatty acid content of plants will modify resistence to drought and attack by insects and content peats. The transgenic plants may also be used as sources of hydroxylated and epoxidized fatty acids useful in the manufacture of e.g. lubricants, anti-slip agents, plasticisers, coating agents, detergents
                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                            Fatty acid omega-hydroxylase; cytochrome P450; transgenic plant; lipid; hydroxylation; epoxidation; oilseed; vegetable oil; crop protection; omega-hydroxy acid; CYP94A6; tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317. .328
/note= "haem-binding domain, corresponds to signature
motif claimed in Claim 2"
                                                                                                  Gaps
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Werck-Reichhart D, Salaun J, Durst F;
                                                                42.0%; Score 47; DB 7; Length 308; 60.0%; Pred. No. 80; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding plant fatty acid hydroxylases.
   specific nucleic acids of the invention.
                                                                                                                                                                                                                                                                                                                                                 Tobacco fatty acid hydroxylase CYP94A6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Fig 26A-B; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                  AAY05901 standard; protein; 510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benveniste I,
                                                                                                                                 4 YKLY--NKNSSSNSTLKNLG 21
                                                                                                                                                                33 YKLVMENRNLSSNSAKKELG 52
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                                                      Query Match
Best Local Similarity 60.0%
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N-PSDB; AAX58405.
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Cabello-Huartado F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana tabacum.
                                     Sequence 308 AA;
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                                                                                                                                                                                                                                                                                  AAY05901;
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Domain
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AAYOS901

JUNAYOS901

AAYOS901

AAYO

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Gape
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Pred. No. 1.2e+02;
5; Mismatches 8; Indels
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RESFRLFDKNGDGSITKKELG 34
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         9908-0148565P
9908-0148565P
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9908-0149426P
9908-0149426P
9908-0149930P
9908-0149930P
9908-0151066P
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ilarity 38.1%;
Conservative
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13-AUG-1999;
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16-AUG-1999;
17-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
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30-AUG-1999;
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31-AUG-1999;
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28-8EP-1999
04-0CT-1999
06-0CT-1999
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25-0CT-1999
26-0CT-1999
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3-SEP-1999;
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5-SEP-1999;
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990S-0139456P

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990S-0139461P

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990S-0139461P

990S-014085P

990S-014284P

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990S-0144332P

990S-0144334P

990S-014538P

990S-014733P

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14 - 70N - 1999;
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18 - 70N - 1999;
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The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nuclectide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisera or a monoclonal antibody raised to infection. (I) and polyclonal antisera or a monoclonal antibody raised to comparising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of infection with P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the coded by it will help to expand our understanding of proteins encoded by it will help to expand our understanding of parasite biology, comparing the vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70038 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection.
antimalarial; malaria; protozoacide; infection; insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%; Score 46; DB 3; Length 332; larity 57.1%; Pred. No. 1.3e+02; Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 371-372; 577pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gardner M,
                                                                                                                                                                                                                                                             98US-0107131P
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YNNNSSNNNTSNNI 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carucci D,
                                                   Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-365347/31
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              HOFFMAN S.
CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 332 AA;
                                                                                                    WO200025728-A2
                                                                                                                                                                                                                                                             05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                 (HOFF/)
                                                                                                                                                                                                                                                                                                                                                                                             (VENT/)
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Matches
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  용
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynucleotide is useful for modulating the gene expression within a cell by PTGS, by introducing the polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell and expressing the nucleic acid segment in the call contacting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant cell to produce a differentiated transformed plant. The sequences shown in ABP81173 - ABP81298 represent the product of a segment of A. thaliana cDNA modulated by PTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleic acid segment useful for modulating gene expression within a cell by posttranscriptional gene silencing, and for augmenting a plant cell genome.
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                                                                                                                                                                                                                                                                                                                 Posttranscriptional gene silencing; PTGS; plant; transformation.
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                                                                                                                                                                                                                                                             Arabidopsis thaliana protein #56 modulated by PTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 53; Page 273-274; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glazov EA, Meins F, Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYGN ) SYNGENTA PARTICIPATIONS AG. (FRIE-) FRIEDRICH MIESCHER INST.
                                                                                                    ABP81228 standard; protein; 324 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-2002; 2002WO-EP003806.
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Query Match
Best Local Similarity 38.1%,
Best Local Similarity 38.1%,
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                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-103337/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABZ42072
                                                                                                                                                                                                                                                                                                                                                                                                                        W0200281695-A2
                                                                                                                                                                                                            27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2002
                                                                                                                                                        ABP81228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 26
                                                                         ABP81228

XXX ABP6

XXX AB
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The invention relates to new Proteus mirabilis polypeptides and polymucleotides. The invention also relates to antibodies against the polypeptides, methods for producing the polypeptides, method of generating vaccines for immunishing an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polymucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Proteus mirabilis polypeptides and polynucleotides, useful as reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as
                                                                                                                                                                                                                                                            Proteus mirabilis infection; bacterial infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 4823; 870pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000US-00543681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0128706P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biocontrol agents for plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|:||| : |||| :
KIYSKNSLTISTLKRV 18
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                                                                                                                                                                                      Bacterial polypeptide #651
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-895291/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                         Proteus mirabilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADF00366
                                                                                                                                                                                                                                                                                                   immunostimulant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS6605709-B1.
                                                                                                            12-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Breton GL;
                                      ADF04538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nad1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB62090

ID AAB6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid models and itself and itself acid; (2) a host cell containing the vector; (3) an isolated of polypeptide acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the gene product itself or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the extent to which each of the strains is present in a culture or collection of product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational and shown of an organism. The antisense molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 51602; 1766pp; English
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1646 FEKNSSNFSKNTLKNIGD 1663
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 YNKNSS--SNSTLKNLGE 22
                                                                                                                                                                                                                                                    21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-0094893.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-0072881.
06-MAR-2002, 2002US-0362699P.
                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-029926/02
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                                  WO200277183-A2
                                                                                                            03-OCT-2002
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Wall D,
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                                                                     Gaps
                                                                     .
40.2%; Score 45; DB 7; Length 60; 56.2%; Pred. No. 23; 3; Indels iive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T. indica Cox1 intronic open reading frame sequence.
                                                                                                                                                                                                                                                                                                                                           AAB62090 standard; protein; 225 AA.
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RESULT 28 ADF04538 ID ADF0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                   Constructing a profile of intronic regions, useful for characterizing organisms e.g. eukaryotes and fungi, comprises selecting intronic regions from nuclear or organellar gene sequences and analyzing the intronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intronic region-encoded protein; IREP; antifungal agent; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.2%; Score 45; DB 4; Length 225; 47.4%; Pred. No. 1.1e+02; ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE30847 standard; protein; 225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytochrome oxidase subunit 1; cox1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tilletia indica coxl IREP protein.
                                                                                                                                                                                                                                               Example 8; Page 59; 69pp; English.
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182 YKTYTKKASSYTTWKEVSE 200
                                                                                                     (CLAR-) CLARITY BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 YKLYNKNSSSNSTLKNLGE 22
                                                      23-AUG-2000; 2000WO-US023119.
                                                                               99US-0150977P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2002; 2002WO-US006069.
                                                                                                                            Honeycutt R, Mcclelland M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                  WPI; 2001-218459/22.
N-PSDB; AAF57219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tilletia indica
          WO200114592-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200277160-A2
                                                                              25-AUG-1999;
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                                  01-MAR-2001
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The invention relates to a method of screening an agent which comprises a nucleic acid coding for a protein that effects intronic region-encoded protein (IRRP)-mediated post-transcriptional processing of RNA. The method involves providing the protein in an assay format adapted for studying the effects of the protein on post-transcriptional processing of pre-mRNA and assaying for the effects in the presence of the agent. The method is useful for producing a composition comprising an agent that modulates IRRP-mediated post-transcriptional processing of RNA for inhibiting growth of a non-human organism, particularly fungus, that is associated with a host organism. The invention is also useful in gene therapy. The present sequence is Tilletia indica cytochrome oxidase subunit 1 (cox1) IRRP protein. This sequence is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                               Screening an agent for modulating cellular activity of a non-human organism, useful for preparing antifungal agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.2%; Score 45; DB 6; Length 225; 47.4%; Pred. No. 1.1e+02; ive 3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG93043 standard; protein; 338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Example 8; Page 57; 68pp; English
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                                                                 (CLAR-) CLARITY BIOSCIENCES INC.
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04-JAN-2001; 2001EP-00870002.
09-JAN-2001; 2001EP-00870003.
01-MAR-2001; 2001US-0272801P.
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                                                                                                                                       Honeycutt R, Ralph
                                                                                                                                                                                                         WPI; 2003-029921/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-667002/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                 N-PSDB; AAD48120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200264766-A2.
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Matches
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This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Baxresistant yeast or fungi, identifying, or obtaining and identifying Baxcandida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The invention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The isotropic activity and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alleviating ascence, or for preventing apportes in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, the sequence represents a polypeptide associated with the Bax gene control of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus, GAS, GBS, group B streptococcus, Streptococcus agalactiae, group A streptococcus, Streptococcus pyogenes, antibacterial, antinflammatory, infection, vaccine, meningitis, gene therapy.
New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.2%; Score 45; DB 5; I 58.8%; Pred. No. 1.9e+02; tive 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ ID NO 5696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP28260 standard; protein; 423 AA
                                                                                             Claim 36; Fig 1; 344pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 YNKANKHVRSSNNTVKN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 YNKNS----SSNSTLKN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pyogenes.
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Best Local Similarity
Matches 10; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-352536/38.
N-PSDB; ABN68891.
                                                       certain diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 338 AA;
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Tettelin H,
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streptococcus/GBS (Streptococcus agalaciae) or group A streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antihilammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactice and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a bilogical sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be maningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
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                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                     The invention relates to a protein (ABP25413-ABP30895) from group B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.2%; Score 45; DB 5; Length 423; 45.5%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori cytoplasmic protein, 10009666.aa.
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                                                                                              Claim 1; Page 3731; 4525pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RSDYKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW20085 standard; protein; 509 AA
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96US-00630405
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus proteins
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N-PSDB; AAT67337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 423 AA;
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01-APR-1996;
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Matches
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               The present sequence is a Helicobacter pylori protein, which may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori nucleic acid sequences and related polypeptide(s) useful for vaccines to treat or prevent H. pylori infection, and to
                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                            Score 45; DB 2; Length 509;
Pred. No. 3e+02;
1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H. pylori transporter protein, 14gp12015orf14.
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                                                                                                                                                                                                                                                                                                                                                                                                           296 YALVGKNASGKSTLINL 312
                                                                                                                                                                                                                                                                                                              40.2%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US009122
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                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 58.00,
                                                                                                                                                                                                                                                                                                                                                                                  4 YKLYNKNSSSNSTLKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith D, Berglindh OT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-052306/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detect Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori
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                                                                                                                                                                                                                                                                          Sequence 509 AA;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cartivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food superprise in tissue, as molecular weight markers and as a food involving aberrant protein expression or biological activity. The involving aberrant protein expression or biological activity. The diagnostics, forensics gene mapping, identifications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences ABGO0010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
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analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                        Length 593;
                                                                                                                                      Score 45; DB 2; Length 593
Pred. No. 3.6e+02;
1; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #14452
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                                                                                                                                                                                                                                                                                                                                                     ABG14461 standard; protein; 657
                                                                                                                                                                                                                                       380 YALVGKNASGKSTLINL 396
                                                                                                                                                                                                                 4 YKLYNKNSSSNSTLKNL 20
                                                                                                                                        40.2%;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631
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Best Local Similarity
Matches 10, Conservat
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                                                                                                 Sequence 593 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
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                                                                                                                                                                                                                                                                                                                RESULT 35
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7177-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human protein, NHP, Wilson's disease, mental disorder;
biological disorder, medical disorder; nootropic, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 40275; 21pp + Sequence Listing, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.2%; Score 45; DB 4; Length 784; 36.8%; Pred. No. 5.1e+02; ive 6; Mismatches 6; Indels
                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 40275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human secreted protein (NHP).
                  ABB71161 standard; protein; 784 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB84950 standard; protein; 996 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::||::||SVLTKNTGAKTILKNMG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 DYKLYNKNSSSNSTLKNLG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD,
                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 784 AA;
                                                                                                                                                                                             pharmaceutical
                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interactions.
                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                                                        ABB71161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB84950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for disgnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                    Gaps
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                                                                                          Score 45; DB 4; Length 657;
Pred. No. 4.1e+02;
2; Mismatches 4; Indels
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41.2%; Pred. No. 4.7e+02;
tive 6; Mismatches 4; IndelB
electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter baumannii protein #1473.
                                                                                                                                                                                                                                                                                                           ADA34312 standard; protein; 733 AA.
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RODFKLMNONTNTEDTI 17
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                                                                                                                60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00328352
                                                                                                                                                                                                             536 RTDYQLYASGSSSRS 550
                                                                                              40.28;
                                                                                                                                                                       1 RSDYKLYNKNSSSNS 15
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                                                                                                                                  9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant biocontrol agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-576092/54.
                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    baumannii protein
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                                                        Sequence 657 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 733 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                    ADA34312;
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plants.

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Gaps

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Homo sapiens

Matches

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RESULT 37

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This represents a novel human secreted protein (MHP) that share structural similarity with animal ceruloplasmins. MHP oligonucleotides are useful as hybridization probes for screening libraries and assessing gene expression patterns. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice in amplification assays to detect mutations within the exons, splice costres, introns that can be used in diagnostics and pharmacogenomics. MHP mucleotide sequences are useful for drug screening and nucleotide construct encoding NHP products are useful in gene therapy for modulating NHP expression and to product an encoding in your of express NHP products in vivo. NHP products e.g. NHP fusion protein products, NHP antibodies and antegonists or agonists are useful as therapeutics i.e., for the treatment of Wilson's disease. The encoded NHP colyppeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                    structural similarity with animal ceruloplasmins, useful for drug
screening, diagnosis and treatment of biological disorders or imbalances.
                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotides encoding human secreted proteins that share
                                            /note= "encoded by RTC"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 26-29; 28pp; English
                                                                                                                                                                                                                   99US-0166429P.
                                                                                                                                                                        16-NOV-2000; 2000WO-US031472
                                                                                                                                                                                                                                                           (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                     Turner CA, Mathur B;
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-355614/37.
                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAF83849.
    Key
Misc-difference
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                                                                                    WO200136469-A2
                                                                                                                                                                                                              19-NOV-1999;
                                                                                                                              25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                New
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Score 45; DB 4; Length 996; Pred. No. 6.8e+02; 5; Mismatches 6; Indels 40.2%; Scor. 42.1%; Pred. No. 5.. 4 YKLYNKNSSSNSTLKNLGE 22 8; Conservative Query Match Best Local Similarity Matches 셤 ઠે

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Gaps

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Secreted protein; SCEP; human; cell proliferative disorder; cancer; keratosis; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis autoimmune disorder; inflammatory disorder; AIDS; arthritis; acquired immunodeficiency syndrome; adult respiratory distress syndrome; Addison's disease; allergy; asthma; osteoporosis; autoimmune thyroiditis; Chohn's disease; dermatitis, diabetes; Graves disease; haemodalalysis; glomerulonephritis; scleroderm; systemic lupus erythematosus; uveitis; systemic sclerosis; ulcerative colitis; infection; trauma; Pick disease; ABG69624 standard; protein; 1049 AA. Human secreted protein SCEP-4. (first entry) 21-OCT-2002 ABG69624; ABG69624

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cardiovascular disorder; congestive heart failure; angina; epilepsy; hypertensive heart disease; neurological disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; stroke; dementia; Huntington's disease; multiple sclerosis; neuromuscular disorder; metabolic disorder; endocrine disorder; toxic myopathy; mental disorder; hypothyroidism; glaucoma; sensorineural disorder; ansemia; epilepsy; transgenic animal.
                                                                                                                                           2001US-0260105P.
2001US-0262932P.
2001US-0263096P.
2001US-0263090P.
                                                                                                                             2000US-0255639P.
2000US-0257852P.
                                                                                                               12-DEC-2001; 2001WO-US048517
                                                                                                                                                                         02-FEB-2001; 2001US-0265926P.
                                                                                 WO200248337-A2
                                                                                                                                         05-JAN-2001; 2
18-JAN-2001; 2
18-JAN-2001; 2
                                                                   Homo sapiens.
                                                                                                                                                                19-JAN-2001;
                                                                                                                             13-DEC-2000;
21-DEC-2000;
                                                                                                20-JUN-2002
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Arvizu C; Griffin JA, Yao MG, Duggan BM, Yue H, Ding L, Lal PG, Lee I Ramkumar J, Thangavelu K, Xu Y, Lee S, Trang YT, Nguyen DB; Warren BA, Honchell CD, Gletzen KJ, Baughn MR, Gandhi AR, Al Walia NK, Lu Y, Elliott VW, Lu DAM, Hafalia AJA, Azimzai Y; WPI; 2002-583509/62. Tran UK; Khan FA,

(INCY-) INCYTE GENOMICS INC.

N-PSDB; ABK99921

Novel human secreted proteins and polynucleotides for diagnosing, preventing or treating cell proliferative, autoimmune/inflammatory, cardiovascular, neurological and developmental disorders.

Claim 1; Page 164-166; 234pp; English

The invention describes an isolated polypeptide chosen from secreted proteins (1), SECP 1-54. (1) and the polynucleotide encoding it (II) are useful for screening a compound for effectiveness as an agonist or compound that alters expression of (II). (I), the identified agonist and antagonist are useful for treating a disease or condition associated altered expression of functional SECP in a patient. An antibody specific to (I) is useful for detecting the presence of (I), puritying (I) from a sample and for diagnosing a condition or disease associated with expression of SECP in a subject or in a biological associated with expression of SECP in a subject or in a biological associated with expression of SECP in a subject or in a biological asmple. (I) and (II) and modulators of (I) are useful for diagnosis, treatment and prevention of cell proliferative disorders (e.g. cancer, keratoris, arterisoclarosis, atheroscierosis, arterisoclarosis, atheroscierosis, atheroscierosc

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Job time : 98.8913 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to multiprotein complexes from eukaryotes. Proteins ABR52568-ABR53003 and ACC6010-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of proteins which is attached thereto from cells. Such protein complexes may comprise up to 30 distinct proteins. Protein complexes of the invention are useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder. Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the European Patent Office. The complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or
                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kruse UD, Kuester BD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 453; 17pp + Sequence Listing; English.
                              Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.2%; Score 45; DB 6; Length 1758;
58.8%; Pred. No. 1.3e+03;
tive 0; Mismatches 7; Indels
                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                         Multiprotein complex; eukaryote; drug target; diagnosis.
                            40.2%; Score 45; DB 5; I
42.1%; Pred. No. 7.2e+02;
iive 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bauer A, Gavin A, Grandi P, Krause R, K
Marzioch M, Schultz JD, Superti-Furga GD;
                                                                                                                                                                                                           ABR52794 standard; protein; 1758 AA.
                                                                                                                4 YKLYNKNSSSNSTLKNLGE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               document is available on CD-ROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-2001; 2001EP-00130253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2001; 2001EP-00111774.
                                                                                                                                                                                                                                                                                                         Protein sequence #SEQ ID 453.
                                                                                                                                                                                                                                                                           (first entry)
                                                               8; Conservative
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae
                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLZOME AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-250078/25.
N-PSDB; ACC60836.
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Sequence 1049 AA;
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                                                                                                                                                                                                                                           ABR52794;
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Search completed: November 24, 2004, 09:21:42

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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November 24, 2004, 09:07:49; Search time 56.663 Seconds (without alignments) 82.302 Million cell updates/sec Run on:

US-09-719-379A-3 72

1 RSDYKFYDNKRID 13 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

Total number of hits satisfying chosen parameters:

2002273

seq length: 0 seq length: 200000000 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:*geneseqp2003bs:* A_Geneseq_23Sep04:* : geneseqp1980s:* geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:* geneseqp20048:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aay79981 Non-typea	Aay79989 Non-typea		Aab47441 LB1(f) co	Aab47445 Entire 3r	Aay79993 Plasmid L	Aay79957 Non-typea	· ·		Aaw67572 Non-typab	Ada25163 H. influe	Adc89652 H. influe	Aay79982 Non-typea	Aay79969 Non-typea	Aay79991 Non-typea		Aay79956 Non-typea	Aay79964 Non-typea	Aay79955 Non-typea	Aab47439 LB1(f) co	Aab20881 LB1gr1 pe		Aaw67581 Synthetic	Aay79986 Measles v	Ada25172 Chimeric
	ΩI	AAY79981	AAY79989	AAY79985	AAB47441	AAB47445	AAY79993	AAY79957	AAY79958	AAY79968	AAW67572	ADA25163	ADC89652	AAY79982	AAY79969	AAY79991	AAY.79965	AAY79956	AAY79964	AAY79955	AAB47439	AAB20881	AAB47443	AAW67581	AAY79986	ADA25172
	DB	m	m	m	4	4	m	m	ო	m	7	ø	7	ო	m	ო	m	ო	m	ო	4	m	4	~	٣	9
	Length	13	13	13	13	22	464	19	19	19	18	18	18	19	19	19	19	19	19	19	19	20	28	40	40	40
фP	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	65.3	61.1	60.4	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7
	Score	72	72	72	72	72	72	47	44	43.5	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
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ALIGNMENTS

Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; onjunctivitis; lower respiratory tract infection. Non-typeable H. influenzae group 3 LB1(f) peptide N1729MEB. AAY79981 standard; peptide; 13 AA. 15-MAY-2000 (first entry) Haemophilus influenzae AAY79981;

W09964067-A2.

16-DEC-1999.

99WO-US011980. 28-MAY-1999; 98GB-00012613. 11-JUN-1998; (SMIK) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS) UNIV OHIO STATE RES FOUND.

×. Lobet Dequesne G, Bakaletz LO, Cohen J,

WPI; 2000-116457/10.

Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.

Example 1; Page 30; 68pp; English.

The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAX79955 to AAX79953, and AAX91201 to AAX291252, represent sequences used in the exemplification of the present invention

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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                    Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                         Non-typeable H. influenzae group 3 LB1(f) peptide N1729MBB.
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                                                                                                                                                                                                                                                                                                                                                                                           Dequesne G,
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13; Conservative
                                           15-MAY-2000 (first entry)
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                                                                                                                                                                                     Haemophilus influenzae.
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              AAY79985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes antigenic PS-like fimbrin subunit peptides (LB1(f) peptides) of PS-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79993, and AAZ91201 to AAZ91202, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                          Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                           Score 72; DB 3; L
Pred. No. 6.6e-06;
Mismatches 0;
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                           Query Match

Best Local Similarity 100.0%;

Matches 13; Conservative 0;
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1es 13; Conservative
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Sequence 13 AA;
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Lobet Y;

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The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various attains. The peptides are used for disgnosis, prevention, and treatment of Heemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. ANT9995 to ANT9993, and AAZ91201 to AAZ91221 represent sequences used in the exemplification of
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Sequence 22 AA;
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                                                                                                                                                                                                                                                                                              Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
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non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
ottis medla; sinusitis; conjunctivitis;
lower respiratory tract infection.
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                                                                                    13-FEB-2001; 2001WO-EP001556
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WO200161013-A1
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Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                  The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein PS, (MOMP PS) of non-typeable H. influenzae (ntHi). Each of these peptides contain an LBI(F) peptide which is a 19 amno acid peptide derived from the sequence of MOMP PS from strain ntHill28, representing amino acids Argll7 to Glyl35. This peptide represents the third exposed loop of PS and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP PS may be used to induce an immune response in a mammal to prevent or treat Haemophilus
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                                                                   Recombinant bacterial outer membrane protein where one or more surface exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY79993 standard; protein; 464 AA.
                                                                                                                                                                                                                                                      Claim 2; Page 26; 29pp; English.
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Matches 13; Conservative
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WPI; 2001-522599/57.
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Pred. No. 0.28;

88.9%;

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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                             RESULT 8
                                                                                                                                                                           AAY79958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes antigenic P5-like fimbrin subunit peptides (LB)(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otils media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAV71955 to AAY7993, and AAX21201 to AAX21202, represent sequences used in the exemplification of the present invention
                                                                   otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
  The present invention describes antigenic P5-like fimbrin subunit peptides (LBI(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzase strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzas infections, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Harding memophilus influenzae; PS-Hike fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; ottiis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                             Length 464;
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                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                         Score 72; DB 3; I
Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY79957 standard; peptide; 19 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                      1 RSDYKFYDNKRID 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenza.
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                                                                                                                                                                                                                      Sequence 464 AA;
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65.3%; Score 47; DB 3; Length 19;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY19955 to AAX79993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine, non-typeable Haemophilus influenzae, ntH1; infection; chimeric protein; Haemophilus influenzae, PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; oritis media; sinusitis; conjunctivitis; lower respiratory tract infection.
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lobet Y;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dequesne G,
                                                                                                                                                                                                                              AAY79958 standard; peptide; 19 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US011980.
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     8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae.
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                                                                                     1 RSDYKFYDD 9
                                                   1 RSDYKFYDN 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-116457/10.
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RSDYKFYEDE
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nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAY-1999;
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ID AAY7
XX
AC AAY7
XX
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The invention relates to the manufacture of a synthetic chimeric peptide comprising a non-typable Haemophilus influenzae fimbrin peptide fused vis a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce an immune response against non-typable Haemophilus influenzae. This sequence represents an example of a H. influenzae fimbrin peptide used to generate the chimeric peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a synthetic chimeric fimbrin peptide. The peptide is useful for treating a non-typable Haemophilus influenzae (NTH) inflection and orlism media. The synthetic peptides do not require tedious purification techniques. The present sequence represents the amino acid sequence of H. influenzae fimbrin subunit peptide #1.
                                                                                                                                 Synthetic chimeric fimbrin peptide - useful for vaccination against non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic chimeric fimbrin peptide, useful for treating Haemophilus influenzae infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fimbrin; non-typable Haemophilus influenzae; NTH1 infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H. influenzae fimbrin subunit peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA25163 standard; peptide; 18 AA.
                                                                                                                                               typable Haemophilus influenzae
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                                                                                                                                                                          Claim 1; Col 3; 16pp; English
                                                                                                                                                                                                                                                                                                                                      59.7%;
77.8%;
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                                                                        Kaumaya PTP, Bakaletz LO
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Matches 7, Conservative
                                           (OHIS ) UNIV OHIO STATE
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                02-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                               Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.
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                                                       Vaccine; non-typeable Maemophilus influenzae; ntHi; infection; chimeric protain; Haemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LBJ(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.4%; Score 43.5; DB 3; Length 19; 55.6%; Pred. No. 1.2; ive 1; Mismatches 0; Indels
                           Non-typeable H. influenzae group 1 LB1(f) peptide N226NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-typable H. influenzae fimbrin peptide #1.
                                                                                                                                                                                                                                                                                                                        Lobet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic composition; immune response.
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                                                                                                                              Haemophilus influenzae
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Best Local S
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Gaps

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Length 18; Indela

Score 43; DB 2; Pred. No. 1.4; 2; Mismatches

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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Hamomophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Hamomophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAZ99255 to AAX79953, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
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                                                                     Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); Immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                     Non-typeable H. influenzae group 1 LB1(f) peptide N1128.
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15-MAY-2000 (first entry)
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Best Local Similarity 77.0
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                                                                                                                                                                    Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel synthetic chimeric fimbrin peptide LB1 or LB2 comprising a first peptide unit, T cell epitope as second peptide unit and third linker peptide unit, useful for preventing or reducing severity of otitis media.
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                   6; Length 18;
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                                                       0; Indels
                 Score 43; DB (
Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                           H. influenzae fimbrin peptide #1.
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                 59.78;
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Best Local Similarity 77.0.
7; Conservative
               Query Match
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Matches 7; Conservative
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(KAUM/) KAUMAYA P T P.
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1 RSDYKFYED 9
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RSDYKFYED
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RESULT 13

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AAY79982 ID AAY7 XX AAY7 AC AAY7

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(OHIS )
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                                                                                                              Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                        The present invention describes antigenic P5-like fimbrin subunit peptides (LBI(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinustis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. Influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
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                                             SMITHKLINE BEECHAM BIOLOGICALS. UNIV OHIO STATE RES FOUND.
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Haemophilus influenza.
                                                                peptides (LBI(f) peptides) of P5-like fimbrin proteins strong various Haemophilus influenzes strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzes infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAX79993, and AAX91201 to AAX91252, represent sequences used in the exemplification of the present invention
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                                                         present invention describes antigenic P5-like fimbrin subunit
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Pred. No. 1.5;
2; Mismatches
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Claim 11; Page 46; 68pp; English.
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Best Local Similarity 77.0
7; Conservative
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antigenic P5-like fimbrin subunit peptides used in vaccines against
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                                                                                             Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                   Non-typeable H. influenzae group 1 LB1(f) peptide NTHI-567.
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Mismatches
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Pred. No.
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77.88;
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                                        15-MAY-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 77.07.77 Conservative
                                                                                                                                                                                                                                                                                                                                                             Bakaletz LO, Cohen J,
                                                                                                                                                                        Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention
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                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-116457/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 AA;
                                                                                                                                                                                                                                                          28-MAY-1999;
                                                                                                                                                                                                                                                                                       11-JUN-1998;
                                                                                                                                                                                                   WO9964067-A2
                                                                                                                                                                                                                                 16-DEC-1999
             AAY79964;
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Best Local $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzes etrains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzes infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzes. Antibodies and probes from the present invention can be used AAZ01201 to AAZ01202, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                    Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                         Gaps
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                            Length 19;
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Pred. No. 1.5;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                           Non-typeable H. influenzae group 1 LB1(f) peptide N152NP.
                                                         Indels
                                                         ;
                            DB 3;
                            Score 43; DB :
Pred. No. 1.5;
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                                                      2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 29; 68pp; English.
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                                                                                                                                                                                       AAY79956 standard; peptide; 19
                         59.78;
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77.8%;
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                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 77.8
Matches 7; Conservative
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen J,
                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae
                                                                                  1 RSDYKFYDN 9
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                                                                                                      RSDYKFYED
                         Query Match
Best Local Similarity
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Sequence 19 AA
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                                                                                                                                                                                                                                                                                                                                                                                                       WO9964067-A2
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                                                         Matches
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ID AAY7
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Gaps

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Length 19; 0; Indels

DB 3;

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WPI; 2000-572040/53
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                                                                                                                                                                                    Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                            AAB20881;
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                                                                                                                                                                                                                                                                                         RESULT 21
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                                                                                                                                      Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                 The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAX79955 to AAX79953, and AAX91201 to AAX91252, represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surface exposed loop; major outer membrane protein P5; MOMP P5;
non-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
otitis media; Binusitis; conjunctivitis;
lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LB1(f) containing peptide from strain ntHi-1128 (Group 1 type).
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                                                                                                                                                                                                                                                                                                        Score 43; DB 3; Length 19;
Pred. No. 1.5;
2; Mismatches 0; Indels
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                                                                                                  Lobet
                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                  Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                            AAB47439 standard; peptide; 19 AA.
                                                                                                                                                                  Example 1; Page 29; 68pp; English
                                   99WO-US011980
                                                      98GB-00012613
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                                                                                                                                                                                                                                                                                                          59.78;
                                                                                                                                                                                                                                                                                                                  77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                 Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae.
                                                                                                                                                Haemophilus influenza.
                                                                                                                                                                                                                                                                      the present invention
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                                                                                                                    WPI; 2000-116457/10.
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                                                                                                                                                                                                                                                                                        Sequence 19 AA;
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                                                                                                  Bakaletz LO,
                                   28-MAY-1999;
                                                      11-JUN-1998;
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                   16-DEC-1999
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AAB47439
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                                                                                                                                                                                                                                 The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein Ps (MOMP Ps) of non-typable H. influenzae (ntill). Each of these peptides contain an LB1(f) peptide which is a 19 amino acid peptide derived from the sequence of MOMP Ps from strain ntHill28, representing amino acids Argl17 to Gly135. This peptide represents the third exposed loop of Ps and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP Ps may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
Recombinant bacterial outer membrane protein where one or more surface-
exposed loops are modified is useful as a vaccine to prevent or treat
Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier; prostate cancer; Haemophilus influenzae; vaccine; infectious disease; malaria; cytostatic; antiallergic; nootropic; neuroprotective; protozoacide; Alzheimer's disease; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%; Score 43; DB 4; Length 19; 77.8%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van-Mechelen MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB20881 standard; peptide; 20 AA.
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                                                                                                                                                                                 Claim 1; Page 26; 29pp; English.
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99GB-00004408.
99GB-00004412.
99GB-00019260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nedia and conjunctivitis.
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RSDYKFYED
                                                                                                                          Sequence 28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                               AAW67581;
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                                              The present invention describes an immunogen (I) comprising a peptide (Ia) and a carrier (Ib) derived from protein D of Haemophilus influenzae or its fragment. Also described are: (I) a vaccine comprising (I), and an excipient; (2) preparation of (I), comprising conjugating a peptide to protein D or its fragment; and (3) preparation of a vaccine of (I), comprising formulating (I) with an excipient. (I) has cytostatic, contraining formulating (I) with an excipient. (I) has cytostatic, nortropic, neuroprotective and protozoacide activities. (I) and the vaccine are useful for the manufacture of a medicament for preventing and treating infectious diseases such as malaria or chronic preventing and treating infectious disease such as malaria or chronic consists and protostatic and the vaccine are timmunogens, (I) induces high levels of antippetide immune responses while inducing a moderate humoral response against the carrier. The present sequence represents an IslgrI peptide which was coupled through an additional C-terminal cysteine via maleimide to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAB47439-46 represent peptides which may be used to replace one or more surface exposed loops of major outer membrane protein P5 (MOMP P5) of non-typeable H. influenzae (ntHi). Each of these peptides contain an LB1(f) peptide which is a 19 amino acid peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant bacterial outer membrane protein where one or more surface-exposed loops are modified is useful as a vaccine to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis
                                                                                                                                                                                                                                                                                                                                Gaps
comprises peptide and carrier from protein D of influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface exposed loop; major outer membrane protein P5; MOMP P5;
on-typeable H. influenzae; ntHi; LB1(f) peptide; B cell epitope;
otitis media; sinusttis; conjunctivitis;
lower respiratory tract infection.
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                                                                                                                                                                                                                                                                                                    59.7%; Score 43; DB 3; Length 20; 77.8%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Entire 3rd loop from strain ntHi-1128 (Group 1 type).
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                                                                                                                                                                                                                                                                                                                              2; Mismatches
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                          Example 14; Page 34; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB47443 standard; peptide; 28 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  media and conjunctivitis.
                                                                                                                                                                                                                                                                                                                 Local Similarity 77.8
ses 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
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1 RSDYKFYED
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  cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the manufacture of a synthetic chimeric peptide comprising a non-typable Haemophilus influenzae fimbrin peptide fused via a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce an immune response against non-typable Haemophilus influenzae. This sequence represents an example of a chimeric fimbrin/T-cell epitope peptide and is designated LBI. The peptide comprises a 19 amino acid sequence corresponding to amino acids 117-135 of the fimbrin protein, the linker sequence and amino acid 208-302 of the measles virus fusion protein (a T-cell epitope)
derived from the sequence of MOMP P5 from strain ntHill28, representing amino acids Argl17 to Gly135. This peptide represents the third exposed loop of P5 and is a potential B cell epitope. The loops of the invention are modified in terms of being in a non-native environment in the recombinant outer membrane protein. The modified MOMP P5 may be used to induce an immune response in a mammal to prevent or treat Haemophilus influenzae infection or associated disease, e.g., otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic chimeric fimbrin peptide - useful for vaccination against non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope; immunogenic composition; immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic chimer fimbrin/T-cell epitope peptide LB1.
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                                                                                                                                                                                                                                                                                                                      59.7%; Score 43; DB 4
77.8%; Pred. No. 2.3;
iive 2; Mismatches
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Pred. No. 3.4;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Col 4; 16pp; English.
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77.8%;
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 77.0
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Best Local Similarity
7, Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSDYKFYDN
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AAY7998

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The invention relates to a synthetic chimeric fimbrin peptide. The peptide is useful for treating a non-typable Haemophilus influenzae (NTH1) inflection and otitis media. The synthetic peptides do not require teditus purification techniques. The present sequence represents the amino acid sequence of the chimeric fimbrin peptide LB1.
                                                                                                                                                                                                                                                                                                                                                   Synthetic chimeric fimbrin peptide, useful for treating Haemophilus

    H. influenzae fimbrin peptide/T cell epitope chimaera LB1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.7%; Score 43; DB 6 77.8%; Pred. No. 3.4; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC89661 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Col 4; 16pp; English
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                                                                                                                                                                                                                                                                                    Bakaletz LO, Kaumaya PTP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 77.8
les 7; Conservative
                             Chimeric.
Synthetic.
Haemophilus influenzae.
                                                                                                                                                                                                                                                 (OHIS ) UNIV OHIO STATE
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Haemophilus influenzae.
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(KAUM/) KAUMAYA P T P.
                                                                                                                                                                                                                                                                                                                                                                     influenzae infections
                                                                                                                                                                                                                                                                                                                     WPI; 2003-615247/58.
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RSDYKFYED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Measles virus.
                                                                                  Measles virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-1998;
otitis media.
                                                                                                                US6436405-B1
                                                                                                                                                                                  14-SEP-1998;
                                                                                                                                                                                                                   02-JUN-1995;
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                                                                                                                                                 20-AUG-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC89661;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
Haemophilus influenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptides (LB16f) peptides) of PS-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract influenzae. Antibodies may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY79933, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                              Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; P5-like fimbrin protein; lipoprotein D; LB1(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes antigenic P5-like fimbrin subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 3; Length 40;
Pred. No. 3.4;
2; Mismatches 0; Indels
                                                                                                                                                                  Measles virus fusion protein T-cell promiscuous epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen J, Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA25172 standard; peptide; 40 AA.
                                                               AAY79986 standard; peptide; 40 AA.
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77.8%;
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                                                                                                                                   (first entry)
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Best Local Similarity 77.0
77.0
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                                                                                                                                                                                                                                                                                    Measles virus
Synthetic.
                                                                                                                                                                                                                                                                                                                                     WO9964067-A2
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                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1999;
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                                                                                                                                   15-MAY-2000
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RESULT 25 ADA2517:

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The fimbrin proteins from 15 randomly selected type b and non- typable
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25-OCT-2001;
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Wall D,
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                                                                               The invention relates to a synthetic chimaeric fimbrin peptide LB1 or LB2 comprises a first peptide unit derived from H. influenzae fimbrin, a second peptide unit containing a reall epitope and a third linker peptide which connects the first peptide to the second. The chimaeric peptide which connects the first peptide to the second. The chimaeric peptide is useful for inducing an immune response in animals against non-typable Haemophilus influenzae (NTHi) and for preventing or reducing adherence of NTHi to host cells thereby preventing or reducing the severity of otitis media. The present sequence is an H. influenzae fimbrin peptide/measles virus T cell epitope chimaeric peptide of the
                  Novel synthetic chimeric fimbrin peptide LB1 or LB2 comprising a first peptide unit, T cell epitope as second peptide unit and third linker peptide unit, useful for preventing or reducing severity of otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine comprising non-typable Haemophilus influenza fimbrin protein - useful in studying, preventing or reducing the severity of otitis media, also fimbrin protein and DNA.
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                                                                                                                                                                                                                      59.7%; Score 43; DB 7; Length 40; 77.8%; Pred. No. 3.4; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Non-typable Haemophilus influenza (NTHi) fimbrin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22. .33
/label= amino terminus
234. .249
/label= internal CNBr fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sirakova
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fimbrin protein; vaccine; otitis media
                                                            Claim 8; SEQ ID NO 10; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         AAR66294 standard; protein; 359 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kolattukudy PE, Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00065442.
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                               Local Similarity 77.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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WPI; 2003-810881/76
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RSDYKFYED
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                                                                                                                                                                                                    Sequence 40 AA;
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09-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                              AAR66294;
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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Matches
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clinical isolates of Haemophilus influenzae share common epitopes. Thus frimbrin isolated from non-typable Haemophilus influenzae 1128 strain is a particularly suitable immunogen to protect against the different non-typable HJ. influenzae that cause otitis media. Fimbrin protein is produced by culturing a transformed microbial host, pref. B.coli, Sporodoptera frugiperda or a mucosal pathogen. Fimbrin protein (FP) produced by this process is claimed. The FP protein migrates in polyacrylamide genes to a posn. equiv. to a mol. wt. of 25.5 kD or 37.5 kD. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct DA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.7%; Score 43; DB 2; Length 359; 77.8%; Pred. No. 39; tive 2; Mismatches 0; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by Prokaryotic essential gene #7962.
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001US-00948993.
2001US-0342923P.
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06-MAR-2002; 2002US-0362699P
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Query Match
Best Local Similarity 77.8°,
Schan
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RSDYKFYED 146
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 359 AA;
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and treatment of Haemophilus influenzae infections, such

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proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits callular proliferation, (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required for the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overaxpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for acidentifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational dentifying proteins or screening for homologous nucleic acids acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. acruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the private of the private and the companies.
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81;
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Pred. No.
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(OHIS ) UNIV OHIO STATE RES FOUND.
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133 RSDYRIFQNRSVD 145
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Best Local Similarity
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            otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY19955 to AAY1993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
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Pred. No. 2.2;
1; Mismatches (
                                                                                                                                                      DB 3;
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Pred. No. 2.2;
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87.5%;
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87.5%;
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                                                                                                                                                                                    7; Conservative
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                                                                                         the present invention
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Matches 7; Conserv
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                                                                                                                         Sequence 19 AA;
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Best Local S:
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15-MAY-2000
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Haemophilus influenza.
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                                                                                                                                      Vaccine, non-typeable Haemophilus influenzae, ntHi, infection, chimeric protein, Haemophilus influenzae, P5-like fimbrin protein, lipoprotein D; LB1(f); immunogenic, antigenic, otitis media, sinusitis, conjunctivitis, lower respiratory tract infection.
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                                                                                                                      Non-typeable H. influenzae protien P5 Group 1 type peptide.
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Pred. No. 3
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                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  Dequesne G,
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                                                               AAY79992 standard; peptide; 19 AA
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87.5%;
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Best Local Similarity 87.5.
Triconservative
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RSDYKFYD 8
          1 RSDYKFYE 8
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                                                                                                                   Vaccine, non-typeable Haemophilus influenzae, ntHi; infection; chimeric protein; Haemophilus influenzae; PS-INke fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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                                                         Non-typeable H. influenzae group 1 LB1(f) peptide NTHI-601.
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Pred. No. 2.2;
1; Mismatches (
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Best Local Similarity
7; Conserve
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Haemophilus influenza.
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                                                                                                                                                Sequence 19 AA;
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                                                                                                                             antigenic P5-like fimbrin subunit peptides used in vaccines against
                                                                                                                                                                                  peptides (LBI(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. AAY79955 to AAY7993, and AAS91201 to AAA291252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine, non-typeable Haemophilus influenzae, ntHi, infection, chimeric protein, Haemophilus influenzae, P5-like fimbrin protein, lipoprotein D; LB1(f), immunogenic, antigenic, otitis media, sinusitis;
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                                                                                                                                                                             present invention describes antigenic P5-like fimbrin subunit
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Pred. No. 2.2;
1; Mismatches 0; Indels
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                                                          BIOLOGICALS
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                                                                                       Dequesne G,
                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGI
(OHIS ) UNIV OHIO STATE RES FOUND.
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87.5%;
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Best Local Similarity 87.5
Eathen 7; Conservative
                                                                                      Cohen J,
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                                                                                      Bakaletz LO,
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                    28-MAY-1999;
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                                                             The present invention describes antigenic P5-like fimbrin subunit peptides (LB1(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzae strains. The peptides are used for diagnosis, prevention, and treatment of Haemophilus influenzae infections, such as otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. influenzae. Antibodies and probes from the present invention can be used for diagnosis of H. influenzae infection. ANY19955 to ANY1993, and AAZ91201 to AAZ91252, represent sequences used in the exemplification of
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Pred. No. 2.2;
1; Mismatches
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Example 1; Page 29; 68pp; English.
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87.5%;
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Best Local Similarity 87.5
Matches 7; Conservative
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Novel antigenic P5-like fimbrin subunit peptides used in vaccines against
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                                                                                                                                                Vaccine; non-typeable Haemophilus influenzae; ntHi; infection; chimeric protein; Haemophilus influenzae; PS-like fimbrin protein; lipoprotein D; LBI(f); immunogenic; antigenic; otitis media; sinusitis; conjunctivitis; lower respiratory tract infection.
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l; Mismatches
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 AAY79963 standard; peptide; 19 AA.
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Best Local Similarity
Matches 7; Conserv
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Pred. No. 2.2;
1; Mismatches 0; Indels
                                                     58.3%; Score 42; DB 3; Length 19; 77.8%; Pred. No. 2.2; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                Non-typeable H. influenzae 10567RM Group 1 type peptide
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87.5%;
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Best Local Similarity 77.8%,
7; Conservative
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                                                                                                                                  1 RSDYKFYDN 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-116457/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RSDYKFYD 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||||
RSDYKFYE 8
                                                                                                                                                        1 RSDYKFYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19 AA;
                   Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9964067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                             15-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-1999.
                                                                                                                                                                                                                                                                                                     AAY79987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 37
AAY79963
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Gaps

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0; Indels

Haemophilus influenzae.

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Length 19;

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Misc-difference
                                                                                                                                                                                                                                                                                                                Sequence 329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP680765-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR85450;
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR85450
a
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                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                             Novel antigenic P5-like fimbrin subunit peptides used in vaccines against Haemophilus influenza.
                                                                                                                                                                                                                            otitis media, sinusitis, conjunctivitis, or lower respiratory tract infection. The peptides may also be used in vaccines against H. Influence. Antibodies and probes from the present invention can be used for diagnosis of H. influencae infection. AAY79955 to AAY7993, and AAS91201 to AAZ91252, represent sequences used in the exemplification of the present invention
                                                                                                                                                                                         The present invention describes antigenic P5-like fimbrin subunit peptides (LBI(f) peptides) of P5-like fimbrin proteins from various Haemophilus influenzas strains. P5-peptides are used for diagnosis, prevention, and treatment of Raemophilus influenzae infections, such as
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allotococcus otitidis; antigenic protein; immunogenic; immunisation; gene therapy; Gram-positive bacterium; infection.
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                Score 42; DB 3; Length 19;
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fletcher LD, Mcmichael JC, Russell DP, Zagursky RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       otitis antigenic protein SEQ ID NO:5654.
                                                                                                           Lobet
                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS (OHIS ) UNIV OHIO STATE RES FOUND.
                                                                                                           Dequesne G,
                                                                                                                                                                                                                                                                                                                                                                                                                  ADB11406 standard; protein; 329 AA.
                                                                                                                                                                         Example 1; Page 29; 68pp; English
                                                                                                                                                                                                                                                                                                                58.3%;
87.5%;
                                            99WO-US011980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-NOV-2002; 2002WO-US036123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-NOV-2001; 2001US-0333777P.
                                                              98GB-00012613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                           Bakaletz LO, Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-505284/47.
N-PSDB; ADB11409.
                                                                                                                            WPI; 2000-116457/10.
                                                                                                                                                                                                                                                                                                                                                  1 RSDYKFYD 8
                                                                                                                                                                                                                                                                                                                                                               ||||||||
RSDYKFYE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alloiococcus otitis
                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003048304-A2.
                                                                                                                                                                                                                                                                                              Sequence 19 AA;
        WO9964067-A2
                                           28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alloiococcus
                                                              11-JUN-1998;
                         16-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB11406;
                                                                                                                                                                                                                                                                                                                Query Match
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The present invention describes an isolated polymucleotide (1) of
Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
an isolated polypeptide that is encoded by the polymucleotide (1), its
complement, degenerate variant or fragment; (3) a genetically engineered
the stansfected, transformed or infected with the vector of (2);
(4) an antibody specific for the polypeptide of (1); (5) an immunogenic
composition comprising the polypeptide of (1); (5) an immunogenic
composition comprising the polypeptide of (1); (6) an immunogenic
composition comprising the polypeptide, its composition comprising the
expression vector; (6) a pharmaceutical composition comprising the
copypeptide of (1) and a carrier; (7) a protein chip comprising the
copypeptide of (1), their biological equivalent or fragment;
cof the polypeptides of (1), their biological equivalent or fragment;
cof the polypeptides of (1), their biological equivalent or has the
cottidia in the biological sample; (10) a kit comprising a container,
containing the novel polymucleotide, its degenerate variant or fragment,
cortining the novel polymucleotide, its degenerate variant or fragment,
cortining the novel polymucleotide, its degenerate variant or fragment,
cortining the novel polymucleotide, its degenerate variant or fragment,
cortining the novel polymucleotide, its degenerate variant or fragment,
cortining the novel polymucleotide, its degenerate variant or fragment
contraining the polympetides, antibodies and compositions of the present
to polymucleotides, polypeptides, antibodies and compositions of the present
cortining assays and monitoring of effects during diagnosing Aug
cortining the persent sequence represente an Alloiococcus
cottidias. The persent sequence represente an Alloiococcus
cottidias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring of effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amino acid at position 195 is not identified in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amino acid at position 311 is not identified in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 6
Pred. No. 53;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   otitidis. The present sequence represents a antigen protein from the present invention.
                                                                                                                                                          Claim 33; SEQ ID NO 5654; 1019pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nontypable H. influenzae P5 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŕ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR85450 standard; protein; 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95EP-00302996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|| | |:|
127 SDFKFQDRSRLD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SDYKFYDNKRID 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
7; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 195
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Nontypable H. influenzae HI outer membrane protein P5 was isolated by extraction of the outer membrane with detergents and cation-exchange chromatography. P5 (or its peptide fragmente) are used in vaccines for prevention of H. influenzae infections implicated in otitis media, sinusitis and chronic pulmonary obstructive disease
                                                                                                                                                 Purified H.influenzae P5 outer membrane protein - used for preventing reducing susceptibility to or treating H.influenzae infections.
                                                                                                                                                                                                  Disclosure; Page 7-8; 16pp; English.
                 94US-00210394.
                                                (AMCY ) AMERICAN CYANAMID CO.
                                                                                                                  WPI; 1995-375029/49.
                                                                                                                                                                                                                                                                                                                                      Sequence 338 AA;
                 05-MAY-1994;
                                                                                 Zlotnick GW;
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0; Gaps Query Match 58.3%; Score 42; DB 2; Length 338; Best Local Similarity 87.5%; Pred. No. 54; Matches 7; Conservative 1; Mismatches 0; Indels ò

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1 RSDYKFYD 8 |||||||: 119 RSDYKFYE 126

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Search completed: November 24, 2004, 09:21:43 Job time : 57.663 secs